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Listing first 45 summaries
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Homo sapiens

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cDNA for the human beta 2-adrenergic receptor: a protein with multiple membrane-spanning domains and encoded by a gene whose chromosomal location is shared with that of the receptor for platelet-derived growth factor proc. Natl. Acad. Sci. U.S.A. 84 (1), 46-50 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3451)

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Homo sapiens (clone: pTF.) (tissue library: Evan Sadler) placenta
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896. .967
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AF202305.1 G
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Rupert, J.L. and Hochachka, P.W. Beta, 2-adrenergic receptor allele frequencies in two
Direct Submission
Submitted (04-NOV-1999) Zoology, University of British
6270 University Blvd., Vancouver, BC V6T 124, Canada
                                                                                                             Unpublished
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1376. .3307
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/note="b-2-adr r
1379. .3383
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AFQELLCLRRSSLKAYGNGYSNONTGEOSGYHVEQEKENKLLCEDLPGTEDFVGHOG
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a 873 c 895 g 893 t
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LAIVEGNVLVITAIAKFERLQTVTNYEITSLACADLVMGHDVPFGAAHILMKMMTFG
NEWCDEWTSIDVLCVTASIETLCVIAVDRYEAITSPEKYQSLLTKNKARDIILMKWMTFG
SGLTSELPIQMHWYRATHQEAINCYANETCCDEFTNQAYAIASSIVSEYVPLVIMVEV
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/protein_id="AAA88015.1"
/db_xref="GI:178202"
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1369. .3383
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/protein_id="AAA88014.1"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1242)
Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B.
Mutations in the gene encoding for the beta 2-adrenergic
in normal and asthmatic subjects
Am. J. Respir. Cell Mol. Biol. 8 (3), 334-339 (1993)
4 (bases 1 to 1242)
Liggett, S.B. and Gre
                                                                                      Amino-terminal polymorphisms of the human beta 2-adrouse receptor impart distinct agonist-promoted regulatory Biochemistry 33 (32), 9414-9419 (1994)
                                                                                                                                                                                                                                Green, S.A., Cole, G., Jacinto, M., Innis, M. and Liggett, S.B. A polymorphism of the human beta 2-adrenergic receptor within the fourth transmembrane domain alters ligand binding and functional
                                   Erratum:[[published erratum 29;33(47):14368]]
                                                                                                                                                                                94043092
                                                                                                                                                                                               properties of the receptor J. Biol. Chem. 268 (31), 23
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/protein_id="AAF17569.1"
/db_xref="GI:6573153"
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/chromosome="5"
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Green, S.A., Turki, J., Innis, M. and Liggett, S.B. Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory propert Biochemistry 33 (32), 9414-9419 (1994)
                                                                                               94043092
                                                                                                                properties of the receptor T. Biol. Chem. 268 (31), 2
                                                                                                                                                  Green, S.A., Cole, G., Jacinto, M., Innis, M. and Liggett, S.B. A polymorphism of the human beta 2-adrenergic receptor within the fourth transmembrane domain alters ligand binding and functional
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Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B.
Mutations in the gene encoding for the beta 2-adrenergic receptor
in normal and asthmatic subjects
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Submitted (04-SEP-1997) Medicine, Univ of Cincinnati,
Ave ML670564, Cincinnati, OH 45267-0564, USA
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/note="Arg16 to Gly F
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a 331 c 326 g
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/product="beta2-adrenergic receptor"
/protein_id="AAB82148.1"
/db_xref="GI:2570527"
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               Green, S.A., Cole, G., Jacinto, M., Innis, M. and Liggett, S.B. A polymorphism of the human beta 2-adrenergic receptor within the fourth transmembrane domain alters ligand binding and functional properties of the receptor J. Biol. Chem. 268 (31), 23116-23121 (1993)
 J. Biol.
94043092
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1242)

Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B.
Mutations in the gene encoding for the beta 2-adrenergic recein normal and asthmatic subjects
in normal and asthmatic subjects
in normal and asthmatic subjects
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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LAIVEGNVLVITAIAKFERLGTVTNYEITSLACADLVMGLAVVEPGAAHILMKMMTFG
NFWCEFWTSSIDVLCVTASIETTCVIAVDRYFAITSPFKYGSLLTKNKARVIILMVWWI
SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
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/notce="Gln27 to Glu polymorphism"
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/protein_id="AAB82149.1"
/db_xref="GI:2570529"
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Green, S.A., Turki, J., Innis, M. and Liggett, S.B.
Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory properties Biochemistry 33 (32), 9414-9419 (1994)
94347707
2 (bases 1 to 1290)
Rupert, J.R. and Hochachka, P.W
Direct Submission
                                              Unpublished
2 (bases 1
                                                                                                                        Rupert, J.R. and Hochachka, P.W.
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1290)
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Submitted (04-SEP-1997) Medicine,
Ave ML670564, Cincinnati, OH 4526
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Liggett, S.B. and Green, S.A.
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29;33(47):14368]]
                                                                             American populations
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AFQELLCLRRSSLKAYGNGYSSSGNTGEOSGYHVEQEKENKLLCEDLPGTEDFVGHOG
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/replace="g"
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OH 45267-0564, USA
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105; Conser
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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AF203386.1 GI:6636495
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6270 Unive
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                                                                                                                                                                                                                           Unpublished
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349 c 3:
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                                                                                                                    Location/Qualifiers
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Emorine, L.J., Marullo, S., Delavier-Klutchko, C., Kaveri, S.V.,
Durieu-Trantmann, O. and Strosberg, A.D.
Structure of the gene for human beta 2-adrenergic receptor:
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Homo sapiens (clone: H-beta-R-[9,10,11].) epidermis DNA.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression and promoter characterization Proc. Natl. Acad. Sci. U.S.A. 84 (20), 6
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1. .3458
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277. .1032
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AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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                                                                                                                                                                                 /note="ORF; putative"
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1 (bases 1 to 1970)
Chung, F. Z., Lentes, K. U., Gocayne, J., Fitzgerald, M., Robinson, D., Kerlavago, A. R., Fraser, C. M. and Venter, J. C. Cloning and sequence analysis of the human brain beta-adrenergic receptor. Evolutionary relationship to rodent and avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 bp upstream of EcoRI site; chromosome 5q31-q32.
                                                                                                                          Submitted (22-SEP-1987) to the EMBL/GenBank/DDBJ databases substantial corrections are reported in [2] Data kindly reviewed (22-SEP-1987) by Kerlavage A.R.
                                                                                                                                                                                  2 (bases 1 to 1970)
Kerlavage, A.R.
Direct Submission
                                                                                                                                                                                                                                                           beta-receptors and porcine muscarinic receptors FEBS Lett. 211 (2), 200-206 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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1264. .2505
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YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mGQPGNGSAFLLAPNGSHAPDHDVTQQRDEVWVVGMGIVMSLIV
LAIVFGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPFGAAHILMKMWTFG
NFWCEFWTSIDVLCYTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
                     /clone_lib="neonatal human brain stem"
178. .1419
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/note="beta-adrenergic receptor (AA 1-413)"
                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="beta-2 adrenergic receptor"
/protein_id="AAA88017.1"
/db_xref="GI:178204"
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/codon_start-1
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                                                                                                            Location/Qualifiers
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1264. .2505
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                                    www.jgi.doe.gov.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that he

* provided by the submittor.

* This sequence will be replaced
                                                                                                                                                                                                                                            2 (bases 1 to 132858)
DOE Joint Genome Institute.
Direct Submission
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 13288)
DOE Joint Genome Institute.
                                                                                                                                                                                                        Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
by the finished sequence as soon as it is available andthe accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
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1952. .1
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1970
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965. .970
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AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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LAIVEGNVLVITAIAKFERLQTVTNYFITSLACADLVMGLAVVPEGAAHILMKMWTFG
NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWIV
SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
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508 c 482 g
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1502. .1507
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1491. .1496
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/db_xref="GI:29373"
/db_xref="SWISS-PROT:P07550"
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5 clone CIT-HSPC_354F19,
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Local Similarity 98.1%;
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1 (bases 1 to 134419)

DOE Joint Genome Institute.
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Homo sapiens chromosome 5 c.
SEQUENCE, 1 ordered pieces.
ACO11324
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing of Human Chromosome
                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 134419: contig of 134419 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40121
                                                                                                                                                                                                                                                                                                                                                                  ww.jgi.doe.gov.
NOTE: This is
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="CIT-HSPC_354F19"
26539 c 25722 g 40476 t
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                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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1. .134419
                                                                                                   /clone="CIT-HSPC_235N17"
28042 c 27433 g 3867
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                 97.0%;
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 Score 102.8; DB 43;
Pred. No. 1.9e-16;
0; Mismatches 2;
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Pred. No. 1.9e-16;
0; Mismatches 2
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                                    Length 134419;
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                                             cagcaaagggacgaggtgtgggtgggtgggcatgggcatcgtcatgt 106
CAGGAACGGGACGAGGCGTGGGTGGGCATGGGCATCGTCATGT 161
          cagcaaagggacgaggtgtgggtggtgggcatgggcatcgtcatgt 106
                                                                                            100;
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Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopitheci
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Amend, A.M. and Guan, X.M.
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QGTYPSDNIDSQGRSCSTNDSLL"
1289. 1320
/gence"B2AR"
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/note="genomic DNA for this receptor sequenced and found
to be identical with the cDNA"
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                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Carnivora; Fissipedia; Felidae; Felis.

1 (bases 1 to 1336)

Cully,D.F., Tremml,G. and Zachwleja,S.
Felia domesticus beta adrenergic receptor subtype 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF192345 1536 bp DNA 27-OCT-1 Fells catus beta-2 adrenergic receptor gene, complete cds. AF192345 GI:6120128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (05-CCT-1999) MRL, Merck & Co.,
Rahway, NJ 07065, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
2 (bases 1
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Felis catus
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                                                                                                                                                                                                                                                                                               342
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IIMGTFTLCWLPFFIVNIYHVIQDNLIFREVYILLNWVGYVNSAFNPLIYCRSPDFRI
AFQELLCLRSSLKAYKOMYSNINSISTDYAGEHSGGPLGQEKDSEVLCEDPPGTENL
ANRQGTVPNDSIDSQGQNGSTNDSLL*
4 24 c 398 g 372 t
                                                                                                                                                                                                                                                                                                                                                                       /note="G-protein coupled receptor; beta adrenergic
receptor subtype 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Felis catus"
/db_xref="taxon:9685"
/note="synonym: Felis domesticus"
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Pred. No. 2.2e-11;
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Multi-specific Bss
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Canine beta-2 adre
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Matches 106
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02-OCT-1997, J00982,
24-MAR-1996; JP-072914.
(DAIN ) DAINIPPON PHARM CO LTD.
(UDAIN ) FURULANT Y KAWASHIMB H
FUJ11 K, FURULANT Y KAWASHIMB H
FP-PSDB; W34320,
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Homo sapiens.
Key
CDS
                                                                                                                           21-DEC-1998 (first entry)
Human beta-2-adrenergic receptor
Beta-2-adrenergic receptor; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel beta-2 adrenalin receptor sub-type - useful for screening for agonists and antagonists and researching asthmatic diseases Disclosure; Page 27-30; 47pp; Japanese.

This sequence encodes the protein of the invention. The protein of the invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 1251-cyanopindrol. The protein can be used screening for agonists and antagonists, which are useful in researching asthmatic diseases.

Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T;
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20-APR-1998 (first entry)
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21-DEC-1998
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Q24323
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Pred. No. 7.3e-23;
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Title: Perfect score:

Scoring table: Sequence: Run

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problem beta2-adrenergic receptor protein beta2-adrenergic receptor (see pisclosure; Page 33-35; 46pp; English.

Pisclosure; Page 34-35; 46pp; English.

Pisclosure; Page 34-35; 46pp; English.

Pisclosure; Page 33-35; 46pp; Pisclosure; Page 4 postifying a portion of each allels may be comprised and pisclosure; Page 4 postions and pisclosure;
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26-FEB-1998; U03908.
03-MAR-1997; US-811441.
(BGHM ) BRIGHAM & WOMENS HO.
BOUShey H, Chinchilli VM, D.
Martin RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        piagnosing asthma patients predisposed to adverse beta-agonist reactions upon regular administration - by identifying patient homozygous for allele encoding Arg at position 16 of
W09735963-A1.
02-OCT-1997.
24-MAR-1995; JP-072914.
27-MAR-1995; JP-072914.
CDAIN ) DAINIPPON PHARM CO L
FUJ11 K, FURUTANI Y, KAWAShi
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Beta-2 adrenalin receptor
Beta-2 adrenalin subtype;
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/note= "xaa=Leu, Ile"
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amino acid change
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Pred. No. 7.8e-23;
Mismatches 0;
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                                                                                                                          Transments for obesity in dogs processed e.g. The sequence was isolated from a cDNA library receptor (RA-Ca-b2) gene. The sequence was isolated from a cDNA library receptor (RA-Ca-b2) gene. The sequence was isolated from a cDNA library receptor (RA-Ca-b2) gene. The sequence was isolated from a cDNA library receptor (RA-Ca-b2) gene. The sequence was isolated from a cDNA library receptor (RA-Ca-b2) gene. The sequence was isolated from a cDNA library receptor constructed from polyA+ RNA purified from dog brown adipose tissue cells. Constructed from polyA+ RNA purified from dog brown adipose tissue cells. The probe was a 600 bp fragment of the coding region of the human beta-3 constructed from covering the region from the initiation codon to adrenergic receptor covering the region from the initiation codon to transmembrane domain 5 (TM5). The full length insert was cloned into M13 cresquencing using primers v30491-v30510. The sequence can then be for sequencing using primers v30491-v30510. The sequence can then be repressed e.g. in a mammalian cell, by subcloning into an expression comparative studies, e.g. for differential screening of ligands specific for RA-Ca-b2 or RA-Ca-b3 (W44933).

Sequence 2679 BP; 577 A; 736 C; 724 G; 642 T;
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Drumare MF, Lenzen G, Pietri-Rouxel
WPI; 98-032136/03.
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02-OCT-1997.
26-MAR-1997; F00537.
26-MAR-1996; FR-003730.
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Pred. No. 1.4e
0; Mismatches
Score 77.2; D
Pred. No. 2.2e
0; Mismatches
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    useful for screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PT Wild type and mutated sequences of Mycobacterium embCAB operon - PT wild type and mutated sequences to treat mycobacterial strains PT and produce antisense sequences to treat mycobacterial infections PS Disclosure; Fig 6A-I; 62pp; English.

CC operon, which determines resistance to the antimycobacterial drug CC ethambutol (EMB). It includes the embA, embC and embb genes that CC encode proteins (see W73052-54) which are the target of action of CC M. smegmatis for EMB. To identify genes conferring EMB resistance, CC a genemic library from a high level EMB-resistant mutant of M. smegmatis was introduced into wild type M. smegmatis mc2155. Four CC overlapping cosmids were identified which conferred a resistant CC overlapping cosmids were identified which conferred a resistant CC esistance was 9 kb (pIMM99). pIMM99 plus 7 kb upstream M. CC smegmatis sequence was dequences revelaing 3 homologous open CC resistance (embC, embB) and 4 additional potential coding CC regions. Wild-type and mutated embCAB nucleic acid sequences are CC usefil as probes used in the diagnosis of drug-resistant CC mycobacteria or to determine the susceptibility of mycobacteria to CC EMB. The nucleic acids are also useful in the treatment of compobacterial infections; anti-DNA or anti-RNA sequences can be CC administered to inhibit embCAB operon mRNA activity (claimed). The CC uncleic acid sequences as vaccines, or to improve existing CC uncleic acid sequences as vaccines, or to improve existing CC uncleic acid sequences as vaccines, or to improve existing CC uncleic acid sequences as vaccines, or to improve existing CC uncleic acid sequences as vaccines, or to improve existing CC uncleic acid sequences as vaccines, or to improve existing CC uncleic acid sequences as vaccines, or to improve existing CC uncleic acid sequences as vaccines, or to improve existing CC uncleic acid sequences as vaccines, or to improve existing CC uncleic acid sequences as vaccines, or to improve existing CC uncleic acid sequences as vaccines.
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Best Local
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V45185;
19-OCT-1998 (first en
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                                      atherosclerosis; congestive
                                                       Nucleotide sequence encoding human cardiac/brain tolloid-like protein ss; human; cardiac/brain tolloid-like protein; hC/BTLP; restenosis;
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(YESH ) UNIV YESHIVA EINSTEIN COLLEGE
Jacobs WR, Musser J, Telenti A;
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Drug resistance; antibiotic resistance; antimycobacterial; ethambutol; embCAB operon; infection; vaccine; therapy; ds
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Location/Qualifiers
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Best Local S
Matches 54
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22-JUL-1998.
23-DEC-1997; 310521.
02-JAN-1997; US-034471.
(SMIK ) SMITHKLINE BEECHAM COAFLECH AN, ELSHOWLDSGY NA, LEMPI; 98-379062/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis
Key
cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       excessive activity is associated with restenosis, atherosclerosis, congestive heart failure, chronic obstructive pulmonary disease, benign prostatic hypertrophy, glomerulconephritis, nephritis, fibrosis, gliosis, cirrhosis and anomalous wound healing (e.g. keloids). Disease or susceptibility to disease related to expression or activity of hC/BTLP can be diagnosed by detecting a mutation in the gene encoding hC/BTLP. Polypeptides and polynucleotides of hC/BTLP can be used in the treatment of the above diseases.

Sequence 5145 BP; 1536 A; 992 C; 1179 G; 1438 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding human cardiac/brain tolloid-like and related products, used for treating and diagnosing, e.grestenosis, atheroscierosis and congestive heart failure
                                                                                                                                            misc_difference
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The human cardiac/brain tolloid-like protein (hC/BTLP) inadequate
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GB virus; HGBV; diagnosis; vaccine; ss.
GB virus isolate C genotype 1.
Location/Qualifiers
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                                           /note= *base 569 is superfluous to sequence and should be deleted to maintain the reading frame for the
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Best Local S
Matches 47
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11-DEC-1996.
07-JUN-1996: 109206.
07-JUN-1995: US-480995.
19-APR-1996: US-629463.
(ABBO ) ABBOTT LAB.
(ABBO ) ABBOTT LAB.
CATTICK RJ. Dawson GJ. Des
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnostic use and vaccine prodn.

Example 1; Page 57-62; 105pp; English.

A previously described large open reading frame (T45828) for hepatitis GB virus (HGBV) isolate C genotype 1 is provided. The availability of HGBV nucleic acid sequences (see also T45836) obtd.

e.g. by PCR amplification, permits the construction of expression vectors encoding antigenically active regions of the HGBV protein (see also W06536). Novel recombinant HGBV polypeptides are useful as immunoassay reagents for HGBV antigens or antibodies. They can also be used in vaccine prodn., to determine clearance of HGBV from an infected patient, and to raise antibodies.

Sequence 9126 BP; 1611 A; 2514 C; 2913 G; 2070 T;
        Oligo.nucleotide(s) specific for hepatitis GB virus-C, useful as probes and primers - for diagnosis, screening blood etc. and design of specific poly; peptide(s)

Example 1; Page 51-56; 96pp; English.

The invention relates to nucleic acid sequences derived from a novel Hepatitis GB virus (HGBV), a form of non-A to-non-E hepatitis, especially the C serotype of the virus. This sequence represents the NS3 region of the virus genome. The probe (corresponding to bases 4245-4432) can be used to detect, by hybridisation, the presence of HGBV-C serotype nucleic acids in a sample following by RT-PCR amplification of the viral genome.
                                                                                                                                                                                                                                                                                                                                                                                                             Fragment of HGBV NS3 genomic region.

Primer; hepatitis GB virus; HGBV; serotype; hybridisation; RT-PCR; LCR; reverse transcriptase; probe; amplification; gap ligase chain reaction; blood; organ; detection; diagnosis; ss.
                                                                                                                                                                         Erker JC, Leary TP, Muerhoff AS, WPI; 97-179430/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T96447 standard; DNA; 9126
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                                                                                                                                                                                                      (ABBO ) ABBOTT LAB.
Birkenmeyer L, Chalmers M,
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14-AUG-1996; U13171.
21-DEC-1995; US-580038.
14-AUG-1995; US-002265.
                                                                                                                                                                                                                                                                                                      WO9708531-A2.
                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis GB virus.
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primers T96445-6.
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Pred. No. 5.
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RESULT 1 V10355/c

AC AC

V10355 standard; DNA; 3919 V10355;

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RESULT 9
V39074/c
ID V39074 standard; DNA; 9126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     petection of hepatitis GB virus - by reacting test samples with primers for amplifying viral RNA primers for amplifying viral RNA Example 1; Page 44-50; 62pp; English.

Example 1; Page 44-50; 62pp; English.

Example 1; Page 44-50; 62pp; English.

Example 2; Page 44-50; 62pp; English.

Example 1; Page 44-50; 62pp; English.

Example 2; Page 44-50; 62pp; English.

Example 3; Page 44-50; 62pp; English.

Example 2; Page 44-50; 62pp; English.

Example 3; Page 44-50; 62pp; English.

Example 3; Page 44-50; 62pp; English.

Example 4; Page 44-50; 62pp; English.

Example 6; Page 44-50; 62pp; English.

Example 6; Page 44-50; 62pp; English.

Example 6; Page 44-50; 62pp; English.

Example 1; Page 44-50; 62pp; English.

Example 2; Page 44-50; 62pp; English.

Example 3; Page 44-50; 62pp; English.

Example 1; Page 44-50; 62pp; English.

Example 1; Page 44-50; 62pp; English.

Example 1; Page 44-50; 62pp; English.

Example 2; Page 44-50; 62pp; English.

Example 1; Page 44-50; 62pp; English.

Example 2; Page 44-50; 62pp; English.

Example 3; Page 44-50; 62pp; English.

Example 2; Page 44-50; 62pp; English.

Example 2; Page 44-50; 62pp; English.

Example 2; Page 44-50; 62pp; English.

Examp
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09-JUL-1998.
23-DEC-1997; U23767.
31-DEC-1996; US-778377.

(ABBO ) ABBOTT LAB.
(ABBO ) ABCTT LAB.
(ABBO ) GJ, Dille BJ, Gutierrez RA, Mushahwar IK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-1998 (first entry)
Hepatitis GB virus E2 gene
HGBV; E2 antigen; immunoass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1152 CGGGCGCCCTTGTGACATGCCCGCCATAGTGACCAGGAGGAAGACCATGACAATACGCT 1093
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1092
                                                                                                                                             1152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in screening procedures for anti-viral agents.
Sequence 9126 BP; 1612 A; 2514 C; 2913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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                                                                                                                                          CGGGCGCGCCTTGTGACATGCCCGCCATAGTGACCAGGAGGAAGACCATGACAATACGCT 1093
                                                                                                                                                                                        cggcagcgccttcttgctggcacccaatagaagccatgcgccggaccacgacgtcacgca 62
GCTCCAGCAGGAGGAGGG 1075
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47; Conservative
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(first entry)

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X1886L7
ID 867
AC X1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PT DNA molecule purified from embryo fibroblasts - useful in, e.g. prinhibiting wound healing abnormalities and treating fibrosis Claim 4; Pages 30-34; 49pp; English.

CC The present sequence is of a human tolloid-like (mTll) cDNA. This cc sequence was derived from clones isolated from a human placenta genomic CC library. The human Tll gene maps to the 4925-4qter region on chromosome CC 4. As the human Tll gene maps to the 4925-dqter region on chromosome CC protein (mTl), it is expected to be a protease having a key role in CC development and homeostatic processes such as wound healing. The CC invention claims that human Tll protein can be used for promoting CC maturation of extracellular matrix precursors into macromolecular CC structures, for activating growth factors in vivo and in vitro and for accelerating developmental and homeostatic processes when administered CC to a tissue. Human Tll protein may also be used to develop inhibitors CC against lite enzymatic activity. Such inhibitors would be useful in CC preventing fibrosis and excess scarring or other abnormalities of wound CC human Tll (W40226) can be used in assays for visualising the production and localisation of mTll protein in cells and tissues.

Sequence 3919 BP; 1089 A; 871 C; 1001 G; 958 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
16-FEB-1999.
25-JUL-1997; JP-200625.
25-JUL-1997; JP-200625.
(TOFU) TONEN CORP.
(MPI; 99-197820/17.
P-SDB; W98969, W98970, W98971, W98972, W98973, W98974, W98975, W98978, W98977, W98978.

New encoding an aromatic cpd. oxidative decompsn. enzyme - useful the fields of petroleum purification, chemical and drug industries claim 1; Page 7-19; J5pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Alcaligenes sp. Pox proteins R, A, B, C, D, E, F, G, H and I coding DNA Alcaligenes; PoxR; PoxA; PoxB; PoxC; PoxD; PoxE; PoxF; PoxG; PoxH; PoxI; aromatic; oxidative; petroleum purification; chemical industry;
                                                                                                                                                                                                                                                                                                                                            Alcaligenes sp.
J11042088-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X18867 standard; DNA; 12019
X18867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WISC ) WISCONSIN ALUMNI RES FOUND. Greenspan DS, Hoffman GG, Takahara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tolloid-like (Tll) cDNA Mammalian tolloid-like; mTll;
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30-MAY-1996; US-018684.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       596 GCGGTCCGCGCTGATGTGCGGGGCTAGGGGCACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAACCCCATCCTCCTCCCCCGGAGGAAAAGGAGGGGACGGGACCCAGAGGTTAGGCAGCC 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Pred. No. 7.7;
0; Mismatches
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Best Local :
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28-JUL-1998.
12-MAR-1997; 815688.
12-MAR-1997; US-815688.
(NEWE ) NEW ENGLAND BIOLABS II
X1ao J, Xu S;
WPI; 98-436530/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes Alcaligenes sp. proteins POXR, POXA POXC, POXD, POXE, POXE, POXG, POXH and POXI. The proteins are us the fields of petroleum purification, chemical industry and drug industry related to the synthesis, conversion and decomposition aromatic compounds.

Sequence 12019 BP; 2015 A; 4104 C; 4151 G; 1747 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multi-specific BssHII methylase enzyme (BssHIIM1) encoding cDNA. Methylase; restriction endonuclease; Bacillus stearothermophilus; enzyme; multi-specific; genetic engineering; ss.
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Key Location/Qua
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509 TCATCGTGGGCATCCGC
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                                    80 gggtggtgggcatgggc 96
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                                                                                    TGTCATGGAAACTCATCAACGCATGGGACTACGGAGTGGCGCAGAAGAGGGGAGCGTGTGT
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59.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Multi-specific BssHII methylase enzyme (BssHIIM1)"
                                                                                                                                                                       Score 27.4; D
Pred. No. 9.1;
0; Mismatches
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Pred.
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RESULT

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PS Claim 1; Page 988; 2245pp; Japanese.
Cd obble-stranded DNA (or its complementary strand or the corresp.
Cd obble-stranded DNA) which comprises one of the 7837 "GS" sequences
Cd 91ven in T19001-T26837 and which is able to hybridise to part of
Cd 91ven in T19001-T26837 and which is claimed. The GS (Gene Signature)
CC 20 chuman genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature)
CC 30 cent of mRNA by using poly(T) as the sole primer. Since the 30 cent untranslated sequence is unique to a particular mRNA species, almost
CC 11 the 30 coriented CDNAs hybridise with specific mRNAs. Each library
CC 12 constructed so as to reflect accurately the relative abundance of
CC 13 constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC crecognising different cell types.
CC Sequence 323 BP; 111 A; 47 C; 63 G; 95 T;
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                   0554 abov.
26-DEC-1995; 537183.
12-UUN-1990; 537183.
12-UUN-1990; US-537183.
02-AUG-1993; US-103739.
28-CCT-1994; WO-U12444.
A (PION-) PIONEER HI-BRED INT INC.
A (PION-) PEONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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WO9514772-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
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                                                                                                                                                                                      10-JUL-1996 (first entry)
Nucleotide sequence for mediating male fertility in plants.
Male fertility; plant; microsporogenesis; tassel development;
maize; sterile; fertile; transformed plant; female parent;
hybrid seed; ds.
                                                                                                                                                      Zea mays.
US5478369-A.
                                                                                                                                                                                                                                                                                         T10928 standard;
   P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                             CCGTGGTCGTCA 104
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44; Conservative
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                                         Howard J,
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detection;
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Search completed: September Job time: 4090 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5824524-A.
20-OCT-1998.
07-JUN-1995; 474404.
02-AUG-1993; US-103739.
12-JUN-1990; US-537183.
07-JUN-1995; US-474404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding a protein critical for male fertility in plants - used to produce plants, esp. maize, that are normally male sterile but can be induced to fertility, esp. for use in hybrid seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prodn
Claim 4; Column 25-27; 27pp; English
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V62709;
24-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PION-) PIONEER HI-BRED INT INC.
Albertsen MC, Beach LR, Howard J, Hu
MPI; 98-582558/49.
P-PSDB; W77413.
Production of male-sterile plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea
                                                                                                                                                                                                                                                                                                                                                                fertility gene
Claim 2; Column 37-40; 40pp; English.
Claim 2; Column 37-40; 40pp; English.
The maize male fertility gene MS45 can be repressed as a method for mediating male fertility in a plant. This method can be used especially mediating hybrid maize seed. The endogenous gene can be inactivated and the control of an inducible promoter can be used to specifically activate the gene when fertile plants are desired.

Sequence 1419 BP; 304 A; 387 C; 473 G; 255 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize male
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38; Conser
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38; Conser
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/note= "No .
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Pred. No. 10;
0; Mismatches
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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PCT-US91-00909-3
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US91/0
FILING DATE: 19910208
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVId J.
REGISTRATION UNUMBER: 91000
REFERENCE/DOCKET NUMBER: 99000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEPAX: 206-622-4900
TELEPAX: 206-622-4900
TELEPAX: 3723836
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1242 base pairs
  Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Ave.

CITY: Seattle

STATE: Washington
COUNTRY: United States
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.

CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sledziewski, Andrzej Z.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Methods of Producing Hybrid
TITLE OF INVENTION: Protein-Coupled Receptors
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear
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US-08-315-486A-20
US-08-317-48-4
US-08-315-486A-20
US-08-317-48-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 990008.408PC
    <u>.</u>.
                     Score 106; DB 6; Pred. No. 4.6e-24;
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    Mismatches
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                                          Length 1242;
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Result

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Minimum Maximum

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PCT-US91-00909-1
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; LOCATION:
PCT-US91-00909-1
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                                RESULT 3
US-08-822-586-46
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/00909

FILING DATE: 19910208

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 990008.408PC

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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GENERAL INFORMATION:
Sequence 46, Application US/08822586 Patent No. 6015890
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                          Query Match
Best Local S
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1254 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Methods of Producing Hybrid G
TITLE OF INVENTION: Protein-Coupled Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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TELEFAX: 3723836
                                                                                                                        61 cagcaaagggacgaggtgtgggtggtgggc 90
                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 CAGCAAAGGGACGAGGTGTGGGTGGGCATGGGCATCGTCATGT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cagcaaagggacgaggtgtgggtggtgggcatgggcatcgtcatgt 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6300 Columbia Center, 701 Fifth Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206-682-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sledziewski, Andrzej Z.
                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                            57.7%;
80.0%;
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Sequence 1, Application US/08991408
Patent No. 6008017
GENERAL INFORMATION:
APPLICANT: ARLETH, ANTHONY J.
APPLICANT: WILLETTE, ROBERT N.
APPLICANT: ELSHOURBAGY, NABIL A.
APPLICANT: LI, XIAOTONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: Ge
; HYPOTHETICAL: NO
US-08-822-586-46
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US-08-991-408-1/c
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Best Local Similarity
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APPLICANT: WIILIAM R. JACOBS, JR., JAMES M. MUSSER AND
APPLICANT: AMALIO TELENTI
TITLE OF INVENTION: AN EMBCAB OPERON OF MYCOBACTERIA AND
TITLE OF INVENTION: MUTANTS THEREOF
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/82,586
FILING DATE: MARCH 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 95700/437
REFERENCE/DOCKET NUMBER: 96700/437
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATII
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb
MEDIUM TYPE: DISKETTE
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ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                9725 TGCAGAGCACCGACACGTGGCAGGACGGCATCAACGGCGGCCTG 9768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9665 ACGCCAACGGCGTCACCGAGGTGCCCAAGTTCCGCCATCTCGCCGGACTACTACGCCAAGC 9724
                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                       TITLE OF INVENTION: HUMAN CARDIAC/BRAIN TOLLOID-LIKE TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               62 agcaaagggacgaggtgtgggtgggtgggcatgggcatcgtcatg 105
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STATE: NEW YORK
                                                 STREET: P.O. BUX >0 CITY: VALLEY FORGE
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COUNTRY: USA
ZIP: 19482
                                       STATE:
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                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61; Conservative
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                                                                         P.O.
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                                                                         RATNER & PRESTIA O. BOX 980
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 Mismatches

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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

IBM Compatible

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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: ATG-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0701
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0:
FILING DATE: 02-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                             TITLE OF INVENTION: Detection of Hepatitis GB
TITLE OF INVENTION: Genotypes
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Rd
                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 CAACCCCATCCTCCCCCCGGAGGAAAAGGAAGGGACGGGACCCAGAAGTTAGGCAGCC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 aagggacgaggtgtgggtggtggcatgggcatcg 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                             STREET: 100 Abbott
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/991,408
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                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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                                                                                     60064
APPLICATION DATA:
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Dosal, S. M
Mushahwar, I.
Chalmers, M.
Dawson, G. J.
                                                                                                    NSD
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                                                                                                                                                                                                                                                                                                                                                                Muerhoff, A. S.
                                                                                                                                                                                                                                                                                                                 Leary,
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ч.
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Pred. No. 1.
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            Version #1.30
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GENERAL INFORMATION:
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                              TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 708-937-03:
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 9126 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1092 GCTCCAGCAGGAGGAGGG 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-0378
                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: POTENDSKI, PT15C111a E.
REGISTRATION UNMBER: 33,207
REFERENCE/DOCKET NUMBER: 5793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                      TELEPHONE: 708-937-0378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR CONTROLLING TITLE OF INVENTION: TRANSLATION OF HEPATITIS GB PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Simons, J. N. APPLICANT: Desai, S. M APPLICANT: Mushahwar, I. K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5793.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 26.8%;
Local Similarity 60.3%;
les 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
STRANDEDNESS:
              TYPE: nucleic acid
                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                               LENGTH:
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; MOLECULE TYPE: US-08-639-857-3
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                                                                                                                                   ; LOCATION: 648..368
; OTHER INFORMATION:
US-08-866-650-4
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                                                            Matches
                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Takahara, Kazuhiko
APPLICANT: HOffman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Greenspan,
APPLICANT: Takahara, I
APPLICANT: Hoffman, G
                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 97094
TELECOMMUNICATION INFORMATION:
TELECPHONE: 608-251-5000
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ORIGINAL SOURCE:
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656 CAACCCCATCCTCCTCCCCGGAGGAAAAGGAGGGGACGGGACCCAGAGGTTAGGCAGCC 597
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                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 648..3689
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                 6 6 cagogoottottgotggocaccaaatagaagocatgogocggaaccacgacgtcacgcagca 65
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                                                             Conservative
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Pred. No. 2.
                                                               Score 27.8; D
Pred. No. 3.3;
0; Mismatches
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Mismatches
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US-09-021-287-4/c
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RESULT 9
US-08-815-688A-2
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Best Local S
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
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NAME: Berson, Bennett J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 53703
                                                                                                                 656 CAACCCCATCCTCCTCCCCGGAGGAAAAGGAGGGGACGGGACCCAGAGGTTAGGCAGCC 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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STREET: 1 South Pinckney Street
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                                                         596 GCGGTCCGCGCTGATGTGCGGGGCTAGGGGCACCG 562
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hes 53; Conserv
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LOCATION: 648..3689
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Pred. No. 3.3;
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US-08-103-739B-1
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                                                                                     Sequence 1, Application US/08103739B Patent No. 5478369
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                           APPLICANT:
APPLICANT:
APPLICANT:
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APPLICATION NUMBER: US/08/815,688A
FILING DATE: 12-MAR-1997
CLASSIFICATION: 435
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TELEPHONE: 508-927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: WILLIAMS, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
   TLE OF INVENTION:
                                                                                                                                                                                            80 gggtggtgggcatgggc 96
                                                                                                                                                                                                                                                       NAME/KEY: Coding Sequence LOCATION: 1...1605
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: WILLIAMS, GREGORY D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: N
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                                                                                                                                                                                                                                                                                               Conservative
                           BEACH, Larry R.
HOWARD, John A.
                                                          ALBERTSEN, Marc C.
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59.7%;
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DNA Sequences Mediating Male Fertility
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Pred. No. 3
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Patent No. 5824524
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APPLICANT: ALBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (515) 248-4844 INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PT C COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,404
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1143 CGAGGACCGGGGCCACGAGGTGATGAAGCTGGTGAGCGAGGTGCGGGAGGTGGGCA 1198
                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleotide Sequences Mediating NUMBER OF SEQUENCES: 8
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APPLICATION NUMBER: US 07
FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                CITY: Des Moines
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FILING DATE: 02-AUG-1993
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HUFFMAN, Gary A
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Pred. No. 4
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APPLICATION NUMBER: FILING DATE: 02-AUG

02-AUG-1993

US 08/103,739

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US-08-474-404-1
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Best Local :
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Patent No. !
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TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
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TELECOMMUNICATION INFORMATION:
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                           TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HOWARD, John A.
APPLICANT: HUFFMAN, Gary A.
TITLE OF INVENTION: Nucleotide Sequences Mediating Fertility and Method of Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                           NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,733 REFERENCE/DOCKET NUMBER: 01 TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248 4897
                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 12-JUN-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 02-AUG-1993 PRIOR APPLICATION DATA:
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ucleic acid
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700 Capital Square, 400 Locust Street
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1419 base pairs
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ER: 0125R2R3
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Pred. No. 4
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ccatgcgccggaccacgacgtcacgcagcaaagggacgaggtgtggggtggtggggca 91

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MOLECULE TYPE:
US-08-485-845-1
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Best Local Similarity
Matches 38; Conserv
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Best Local Similarity
Matches
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
FILING DATE: 02-AUG-
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MEDIUM TYPE: Floppy
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STRANDEDNESS: doubl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Des Moines
STATE: Iowa
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                                                                                                                                                                                                                                    NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,73
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milarity 67.9%;
Conservative
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700 Capital Square, 400 Locust Street
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Conservative
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               25.7%;
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Pred. No. 4.3;
               Score 27.2; D. Pred. No. 4.3;
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    Mismatches
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                                 DB 3;
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US-08-648-657-14

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RESULT 15
PCT-US95-14418-3
Sequence 3, Application PC/TUS9514418
GENERAL INFORMATION:
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AMAE: WALDURY, RICHARD J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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Patent No. 5885813
GENERAL INFORMATION:
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Best Local
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APPLICANT: MOffett, R. Bruce
APPLICANT: Fuller, Carl W.
TITLE OF INVENTION: THERMOSTABLE |
TITLE OF INVENTION: POLYMERASES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOPTWARE: WORD PORFECT 5.1
CURRENT APPLICATION DATA:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                              1366 AGGCGCTACGTGCCCGACCTCAACGCCCGGGTGAAGAGCGTCAGGGAGGCCGCGGAGCGC 1425
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PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION UMBER: US 08/455,686
FILING DATE: May 31, 1995
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Similarity 60.0%;
45; Conservative
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Search completed: September 12, Job time: 3935 sec

2000, 23:04:28

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NAME: GASS, DAVID A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 2800
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312,474-6300
TELEFAX: 312,474-0448
TELEFAX: 312,474-0448
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                 Query Match
Best Local Similarity
Matches 45; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOR COMPATION OF THE COMPATION OF THE COMPATION OF THE COMPATION OF THE COMPATION DATA:
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: DNA
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                         1534 ATGGCCTTCAACATG 1548
                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                    TOPOLOGY: 11
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CITY: Chicago
STATE: Illinoi
                  91 atgggcatcgtcatg 105
                                                                                                                                                                                                         NAME/KEY:
                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                              LENGTH: 1794 base pairs
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6300 Sears Tower, 233 South Wacker Drive
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                                                                                                                single
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 1000000
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September 12, 2000, 21:43:38; Search time 1893.64 Seconds (without alignments) 246.848 Million cell updates/sec
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cm_est3:
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9b_est112:*
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Compugen Ltd.
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Result
                   RESULT
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       DEFINITION
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C18250 377 bp mRNA EST UZ-OCIT-1990 C18250 Human placenta cDNA (TFUjiwara) Homo sapiens cDNA clone GEN-559E06 5', mRNA sequence.
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AU063240
AI347556
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AW185521
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                                                     ALIGNMENTS
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A1661315 val5f07.x
AA470234 vd99h08.r
AV055159 AV055159
AV254331 val5f08.r
AV129231 aV159211
AV129231 aV129211
AV129231 aV129218
AV297381 AV298968
AV297381 AV297381
AV107772 AV107772
AV340114 AV340114
                                                                                                                                                                       AA515527 nf69912.s

AV302729 AV302729

AA980400 ua52910.r

AL135598 DKF7p762E

AV323541 AV323541

AA980836 ua46c02.r

AI021469 ub08f07.r

AA616441 vo09f04.r

AW185521 se80h01.y

AA458282 vy48611.r

T54325 ya91d10.s

A1843984 UIT-M-AP1-
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AA6077055 vm95e04.r
AQ877048 V120F11 m
AV352055 AV352055
AV138058 AV138058
AW225456 SWYD25CAU
AQ858041 nbeb0011N
AA515527 nf69g12 s
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AU063749 AU063749
AU063240 AU063240
AI347556 qc98g12.x
AV157571 AV157571
AW708048 a8h1lne.r
AI329823 b8f10ne.r
                                                                          AW671056 LG1_284_E
AA278503 zs81e04.r
A1706391 UI-R-AE1-
C29133 C29133 Rice
AA218070 mv01g03.r
C93520 C93520 Rice
AW252709 UI-R-BJ0-
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AUTHORS
                                                                                                                                                             ACCESSION
VERSION
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ORGANISM
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                                                                                                                                                                                                               RESULT
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JOURNAL
                                                                                                                                                     KEYWORDS
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Best Local S
Matches 98
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                                                                TITLE
JOURNAL
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ACCESSION
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KEYWORDS
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Unpublished (1996)
Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka pharmaceutical Co.,Ltd
463-10 kagasuno Kwauchi-cho, T
Tel: 0886-65-2888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C18250
C18250.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
1 (bases 1 to 377)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 0886-37-1035.
                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Muridae; Muridae;
Mammaila; Eutheria; Rodentla; Sciurognathi; Muridae; Muridae;
1 (bases 1 to 744)
1 (bases 1 to 744)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub
Marra, M., Hillier, L., Allen, M., Le, M., Martin, J., Morris, M.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA980445 744 bp mRNA EST 2 7 MA 100 A4980445 2 1 MAGE: 1349283 5 Similar to gb: M15169 BETA-2 ADRENERGIC RECEPTOR
                                                        Unpublished (1996)
On Apr 7, 1998 this sequence version replation contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. LC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMAN);, mRNA sequence.
                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA980445.1 GI:3158981
                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                               Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9666"
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/clone_1ib="Human placenta cDNA (TFujiwara)"
/tissue_type="placenta"
/tissue_type="placenta"
/tissue_type="lacenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:1579852
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1. .377
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90.7%;
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Primates;
                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81.2; DI
Pred. No. 2.9e:
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 21 (bases 1 to 165)

E 1 (bases 1 to 165)

Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukunda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Shibata, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Contact: Yoshinide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Lahoratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 aacggcagcgccttcttgctggcacccaatagaagccatgcgccggaccacgacgtcacg 60
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h quality sequence stop: 494.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1349283"
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/dev_stage="4 weeks"
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s (Pharmacia), digested with Not I and cloned into
I and Eco RI sites of the modified pT7T3 vector.
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Pred. No. 5.3e-14;
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
           AA209561 255 bp mRNA EMUTINOS:r1 Soares mouse lymph node NbMLN IMAGE:6444889 5', mRNA sequence.

AA209561 AA209561
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AA209561.1 GI:1807898
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                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

Waterston, R.

The WashU-HHMI Mouse EST Project
                                                                                 A1661315 286 bp mRNA FWA15677.x1 Soares mouse lymph node NbMLN IMAGE:723013 3', mRNA sequence.
A1661315
                                       AI661315.1 GI:4764898
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Mus musculus
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h quality sequence stop: 246.
Location/Qualifiers
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a 68 c 72 g 54 t
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with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
ist strand cDNA was primed with a Not I - oligo(dT) primer
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/dev_stage="4 weeks"
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/clone="IMAGE:644889"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32.8;
Pred. No. 4
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                         CCATGGAGGCCAGGTGCCAGACCCCCAAGGGAAGCAGCCCCGGTCGGGGGGTGGGGGTGGG 127
                                                                                                                                                                                                                                                                                                                               GGAGTGGGGCAAGGTC 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
On Jun 22, 1998 this sequence version replaced g1:3247027.
Other_ESTs: va15f07.yl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Šteptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999

The WashU-NCI Mouse EST Project 1999
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                     vd90h08.rl Soares
                                                                                                                                                                                                               AA470234
                                               Mus musculus
                                                                                                                    AA470234.1
                                                                                                                                       AA470234
                                                                                                                                                             5', mRNA sequence.
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This clone
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                       house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

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with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
ist strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:723013"
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/lab_host="DH10B"
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/sex="male"
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                                                                                                                  GI:2197543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.9%;
                                                                                                                                                                                                               370 bp
                                                                                                                                                                                       mouse
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Pred. No. 4.2;
                                                                                                                                                                                         HMdN
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RESULT 7
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Mus musculus
Eukaryota; Motazoa; C
Mammalia; Eutheria; R
'hages 1 to 172)
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                                                                                                                                                                                                                                                                                              caatagaagccatgcgccggaccacgacgtcacgccagcaaagggacgaggtgtggggtgt
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AV055159
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On Jan 19, 1998 this sequence version replaced g1:2151946.
On Jan 19, 1998 this sequence version replaced g1:2151946.
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                          1 Similarity
49; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                AV055159 Mus musculus pancreas C57BL/6J adult Mus musculus clone 1810034A24, mRNA sequence.
                                                                                        AV055159.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vector to vector length is 371 seq primer: -28ml3 rev2 ET from Amersham.
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                                                         house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH108"
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a 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:807903"
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                                                                                        GI:5154906
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               Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                    AA254331 233 bp mRNA
val5f08.rl Soares mouse lymph node
IMAGE:723015 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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On Apr 3C, 1999 th
Contact: Chie Owa
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 233)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
The WashU-HHMI Mouse EST Project Unpublished (1996)
Contact: Marra M/Mouse EST Projec
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AA254331.1 GI:1888943
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/dev_stage="adult"
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/clone="1810034A24"
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Pred. No.
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Best Local S
Matches 47
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                                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashIn-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
RIKEN Mouse ESTs
Unpublished (1999)
On Aug 21, 1998 thi
Contact: Chie Owa
                                                                        Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Akahira,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Hara,A., Hayatsu,N., Kojima,Y., Matsuyama,T., Nitsuma,H., Oda,H. Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Nitsuma,H., Oda,H. Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Sugahara,Y., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                             AV129211 178 bp mRNA EST AV129211 Mus musculus C57BL/6J 11-day embryo Mus clone 2700066J24, mRNA sequence.
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 178)
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  Aug 21, 1998 this sequence version replaced gi:3707190 stact: Chie Owa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo." 73 c 65 g 52 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:723015"
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/dev_stage="4 weeks"
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Pred. No. 11
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musculus cDNA
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AUTHORS
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AV298968/c
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JOURNAL
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                                                                                                                                                                                              RS Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukuda, S., Tukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Matsuyama, T., Miki, R., Mizuno, Y., Saho, M., Sato, K., Shibata, Y., Shibata, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Shibata, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Yoshino, M., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Riken Mouse ESTS (Konno, H., et al.)

On Oct 30, 1998 this sequence version replaced gi:3816340.

On Oct 30, 1998 this sequence version replaced gi:3816340.

Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@rtc.riken.go.jp
Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
Trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(7):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
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Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                               The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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/strain="C57BL/6J"
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/clone="2700066J24"
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50 c 47 g 43 t
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URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
Mus musculus
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                         AV297381 243 bp mRNA EST AV297381 RIKEN full-length enriched, 8 days CDNA Clone 5730448106 3', mRNA sequence.
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M. Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
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AV297381.1
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                                                                      house mouse.
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/lab_host="DH10B"
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Pred. No. 12;
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Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kkuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Kai, C., Kawai, J., Kkuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Watsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Sighata, Y., Shibata, Y., 
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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Unpublished (1999)
On Jun 15, 1998 this sequence version replaced gl:3224201.
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
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3-1-1 Koyadal, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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                                                                                                                                                                                                                                                                                         /note-"Site_1: Sall; Site_2: BamHI; cDNA library was /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of subtraction to Rot = 100.0 Second strand cDNA was prepared with the primer adapter of sequence [5'
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                                      /organism-"Mus musculus"
/strain-"C57BL/6J"
/db_xref-"taxon:10090"
/clone-"5730448I06"
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                                              gggcatgggcatcgtc 102
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-resertc.riken.go.jp
Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes k
Thermostabilization and thermoactivation for the synthesis of full length cDN
trehalose and its application for the synthesis of full length cDN
(Proc. Natl. Acad. Sci. U.S.A. 95(7):520-524 (1998))
(Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Contact: Chie Owa
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47; Conserv
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                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                45
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="2510040L09"
/clone_1ib="Mus musculus liver C57BL/6J 13-day embryo"
                                                                                                                                                                                                                                                                                                                                                                /tissue_type="liver"
/dev_stage="13-day embryo"
/dev_stage="49 g 43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AV340114
AV340114.1 GI:6380166
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Sasaki.N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse
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Tel: +81-298-36-9913
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olfactory brain"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RIKEN full-length enriched, adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                           /tissue_type="olfactory brain"
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                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                               /clone="6430513A21"
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Yoneda, Y.,

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RESULT 14
A1838527/c
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AUTHORS
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                                                                                                                                                                                                                          The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized prefrontal cortex library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI838527 305 bp mRNA EST 1.
UI-M-ALO-abp-a-12-0-UI.sl NIH_BMAP_MCO Mus musculus
UI-M-ALO-abp-a-12-0-UI 3', mRNA sequence.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Feb 24, 1999 this sequence version replaced gi:4061710. Contact: Chin, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20892-9643, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            discovery
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                   /strain="C57BL/6J"
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/clone_11b="NIH_BMAP_MCO"
/dev_stage="27-32 days"
/lab_host="DH108 (Life Technologies)"
                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                      Location/Qualifiers
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
On Jan 14, 1998 this sequence version replaced g1:1877600.
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA607055 354 bp mRNA EST vm95e04.r1 Knowles Solter mouse blastocyst Bl Mus clone IMAGE:1006014 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 354)
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83 c 81 g 78 t
/note="Organ: embryo; Vector: pSPORT; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally from mRNA prepared
from 800 blastocysts. primer: Sali(dT):
5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTT-3'. cDNAs were
                                                                                         /strain="B6D2 F1/J"
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                                                                                                                                                                                                                                                          /organism="Mus musculus"
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cloned into the NotI/SalI sites of a pSPORT vector (Life

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Technologies). Two different size selections: B1 (larger inserts) and B3."

BASE COUNT 78 a 95 c 101 g 80 t

ORIGIN

Query Match 27.9%; Score 29.6; DB 28; Length 354;

Best Local Similarity 61.8%; Pred. No. 37;

Best Local Similarity 61.8%; Pred. No. 37;

Matches 47; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Matches 47; Conservative 10; Mismatches 29; Indels 0; Gaps 0;

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Mismatches 29; Indels 20; Mismatches 29; Indels 20; Gaps 0;

Mismatches 29; Indels 20; Mismatches 29; Indels 20; Mismatches 29; Indels 20; Mismatches 20; Mismatche
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 1000000
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1: gb_bal: *

2: gb_bal: *

4: gb_ov: *

6: gb_ph: *

6: gb_ph: *

9: gb_pr: *

9: gb_pr: *

11: gb_ov: *

12: gb_ov: *

12: gb_ov: *

13: gb_ov: *

14: gb_y: *

15: gb_un: *

16: em_hum1: *

10: em_ov: *

11: em_ov: *

11: em_ov: *

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12: em_bi: *

13: em_bi: *

14: em_bi: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AC022441 Homo sapi	AF-06/845 HOMO Sap1		AL133435 Leishmani	AF031898 Pseudomon	Y18605 Mycobacteri	AF057063 Erwinia c	AL116199 Botrytis	AL111952 Botrytis	AC011334 Homo sap1	ACO11354 Homo sapi	J02960 Human beta-	M15169 Human beta-	Y00106 Human gene	X04827 Human mRNA	L38905 Macaca mula	AF203386 Homo sap1		AF202305 Homo sap1	AF022956 Homo sap1	AF022955 Homo sap1	. AF022954 Homo sapi	AF022953 Homo sap1	Description

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KEYWORDS
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3 (creen, S.A., Turki, J., Innis, M. and Liggett, S.B., adrenergic Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory propert Biochemistry 33 (32), 9414-9419 (1994)
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                                                                                                   ocation/Qualifiers
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3035
4928
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the beta 2-adrenergic
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AF134836 Mus muscu
X94608 C.familiari
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AE000106 Rhizobium
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U95094 Xenopus lae
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/gene="ADRB2" /codon_start=1

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Liggett, S.B. and Green, S.A.
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
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Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory propert Biochemistry 33 (32), 9414-9419 (1994)
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A polymorphism of the human beta 2-adrenergic receptor within the fourth transmembrane domain alters ligand binding and functional properties of the receptor
J. Biol. Chem. 268 (31), 23116-23121 (1993)
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Mutatlons in the gene encoding for the beta 2-adrenergic receptor
in normal and asthmatic subjects
in J. Respir. Cell Mol. Biol. 8 (3), 334-339 (1993)
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
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19; Conser
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Location/Qualifiers
1. .1286
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1 (bases 1 to 1286)
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Homo sapiens beta-2 andrenergic receptor gene, complete
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ILMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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Newceewtsidvlcvtasietlcviavdrybaitspexyqsllknkabvilavveiv
Sgliselpiqmwyrathqbaincyanetccdeftndayaiassivseyvplvimvev
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YSRVFOBAKROLOKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
IIMGTETLCWLPFFIYNIVHYIQDNLIRKEVYILLMNIGYVNSGFNPLIYCRSPDFRI
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                                                                                                                                                                                                                                         /product="beta-2 andrenergic receptor"
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/chromosome="5"
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               1 aacggcagcgccttcttgc 19
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Rupert, J.R. and Hochachka, P.W.
Direct Submission
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Rupert, J.R. and Hochachka, P.W.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                  /Chromeson---
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SGLXSELPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSEYVPLVIMVEV
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349 c 3
                                                                                                                                                                                                           AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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AF203386.1 G
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Macaca mulatta beta-2 adrenergic receptor (B2AR) mRNA, complete
                                                                     L38905.1 GI:1004338
beta-2 adrenergic receptor.
Macaca mulatta cDNA to mRNA.
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Rupert, J.L. and Hochachka, P.W.
Beta 2 adrenergic receptor allele frequencies in two
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1 (bases 1 to 1320)
Amend, A.M. and Guan, X.M.
                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
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/sex="female"
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/db_xref="taxon:9606"
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                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1970)
Chung, F. Z., Lentes, K.U., Gocayne, J., Fitzgerald, M., Robinson, D., Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
Cloning and sequence analysis of the human brain beta-adrenergic receptor. Evolutionary relationship to rodent and avian beta-receptors and porcine muscarinic receptors
EEBS Lett. 211 (2), 200-206 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning, sequencing, and expression of the rhesus monkey beta adrenergic receptor DNA Cell Biol. 14 (9), 753-757 (1995) 95398843
                                                 Direct Submission
Submitted (22-SEP-1987) to the EMBL/GenBank/DDBJ databases
Substantial corrections are reported in [2]
Data kindly reviewed (22-SEP-1987) by Kerlavage A.R.
                                                                                                                                                                                                                                                                                                                                                                                                     X04827
X04827.1 GI:29372
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Kerlavage, A.R.
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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LAIVEGNVLVITAIAKEERLQTVTNYEITSLACADLYMGLAVVEPGAAHILMKMMTEG
NEWCEEWTSIDVLCVTASIETLCVIAVDRYEAITSPEKYGSLITKNKARPULILMVWYFV
SGLTSELPIOMHWYAATHQEAINCYAKETCCDFFTNOAYAIASSIVSFYVPLVIMVFV
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41. .1288
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1289. 1320
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IIMGTFTLCWLPFFIVNIVHVIQDNLIPKEVYILLNWVGYVNSGFNPLIYCRSPDFRI
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/product_"beta-2 adrenergic receptor"
/protein_id="AAC41914.1"
/db_xref="GI:1004339"
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/db_xref-"taxon:9544"
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/organism="Homo sapiens"
                                ocation/Qualifiers
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1 Similarity 100.0%;
19; Conservation
                                                                                                                                                                   Direct Submission submitted (20-OCT-1987) to the EMBL/GenBank/DDBJ databases
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Schoffeld, P.R., Rhee, L.M. and Peralta, E.G.
                                                                                                                                                                                                    Schofield, P.R.
                                                                                                                                                                                                                                     87203400
                                                                                                                                                                                                                                                   Primary structure of the human beta-adrenergic receptor gene Nucleic Acids Res. 15 (8), 3636 (1987)
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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gene for beta-adrenergic
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1502. . ]=^:
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1952. .1957
/note="pot. polyA signal"
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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kalvegnvlyItalakferlotytnyfitslacadlymglaytychychabhilmkmyfeg
Newcefwtsidvlothasieficvlavdryfaltsprygaslitknyapytlylmyfy
Sglisflþommykathqeaincyametccdfftnqayaiassiysfyvplyimyfy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="neonatal human brain stem"
178. .1419
/note="beta-adrenergic receptor (AA 1-413)"
                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Maniatis human"
/clone="lambdahbetaAR17"
                                                                                                                                  Location/Qualifiers
1. .2305
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508 c 482 g
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/protein_id="CAA68289.1"
                                 /note="beta-adrenergic receptor (AA 1 -
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.1507
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.1464
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                                                                                                                                                         Kobilka, B.K., Dixon, R.A., Frielle, T., Dohlman, H.G., Bolanowski, M.A., Sigal, I.S., Yang-Feng, T.L., Franck and Lefkowitz, R.J.
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3451)

Kobilka, B.K., Frielle, T., Dohlman, H.G., Bolanowski, M.A., Dixon, R.A., Keller, P., Caron, M.G. and Lefkowitz, R.J.

Delineation of the intronless nature of the genes for the human and hamster beta 2-adrenergic receptor and their putative promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human beta-2-adrenergic receptor mRNA, complete M15169 J02728 M16106 M15169.1 GI:178201
                                                                          cDNA for the human beta 2-adrenergic receptor: a protein with multiple membrane-spanning domains and encoded by a gene whose chromosomal location is shared with that of the receptor for platelet-derived growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adrenergic receptor.
Homo sapiens (clone: pTF.) (tissue library: Evan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA to mRNA.
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                                                                                                                                                                                                                                                                  Biol. Chem. 262 (15),
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/translation="MGOPGNGSAFILAPNRSHAPDHDVTQQRDEVWVVGMGIVMSLIV/translation="MGOPGNGSAFILAPNRSHAPDHDVTQQRDEVWVVGMGIVMSLIVLAIVFGNVLVLTAIAKERLQTVNFTTYSLACADLVMGLAVVPFGAAHILMKMWTFGNFWCEFWTSLDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWTVSGLTSFLPIQMYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFVSGLTSFLPIQMYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"membrane spanning domain VI"
1712. 1774
/note-"membrane spanning domain VII"
616 c 649 g 545 t
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1007. .
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TYPSDNIDSQGRNCSTNDSLL"
Location/Qualifiers
1. .3451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="membrane spanning domain IV" 1385. .1450
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1114. .1180
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IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="membrane spanning
1616. .1687
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1247. 1315
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                       AACGGCAGCGCCTTCTTGC 1621
                          Emorine, L.J., Marullo, S., Delavier-Klutchko, C., Kaveri, S.V. Durieu-Trautmann, O. and Strosberg, A.D. Structure of the gene for human beta 2-adrenergic receptor:
                                                                                                                                adrenergic receptor; beta-2 adrenergic receptor. Homo sapiens (clone: H-beta-R-[9,10,11].) epidermis
expression and promoter characterization Proc. Natl. Acad. Sci. U.S.A. 84 (20), 6
                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3458)
                                                                                                                                                                J02960.1 GI:178203
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873 c 895 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="beta-2 adrenergic
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/note="b-2-adr mRNA (alt.); G00-120-541"
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1369. .3383
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/db_xref="taxon:9606"
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/note="b-2-adr
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/tissue_lib="Evan Sadle
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 132858)
DOE Joint Genome Institute.
                                                                                                                  AC011354.1 GI:6013586
HTG; HTGS_PHASE2; HTGS_DRAFT
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AC011354
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Homo sapiens chromosome 5 clone
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Sequencing of Human Chromosome
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GRVFTFCVCHHVFVLLGASVFYSGRVSVLDRGDFVPDGFCVRARASVHYGELGGCVSV
SMAVVRYKSEHVCQGVFVPVCACLGGHSRFLPNVGQCRCAALCLETSSRAGAQGRQVA
ATEEPKAPGLAGKHTTSSFSPLGPARVAGKQMPALQGAVGPRPGQPQEKEGEGRGGK
GEECLAPSRLPACHWPKVPVRHGEGSSPKVLCT"
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/map="5q31-q32"
277. .1032
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1055. .3057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQC
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1264. .2505
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/cell_line="A431"
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/db_xref="taxon:9606"
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Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
www.jgi.doe.gov.

* NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.

* This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 1161: contig of 1161 bp in length
gap of unknown length
and of 132858: contig of 72327 bp in length.

Location/Qualifiers
Location/Qualifiers
**NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* the accession number will be preserved.

* the accession number will be preserved.

* Location/Qualifiers
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DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC011334 134419 bp DNA HTG Homo sapiens chromosome 5 clone CIT-HSPC_235N17,
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 134419)

DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE, 1 ordered pieces. ACO11334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC011334.1 GI:6013606
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                   Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                www.jgi.doe.gov.
                                                                                                                                                                                                                                                                                                                      Direct Submission
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DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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/db_xref="taxon:9606"
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1 (bases 1 to 720)
Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.
Direct Submission
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
(bases 1 to 720)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA library; nitrogen deprivation.
Botryotinia fuckeliana.
Botryotinia fuckeliana
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Botrytis cinerea strain
                                                                                                                                                                                                                                                                                                                                                                                     Web: www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this project was created using a Botrytts cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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/db_xref="taxon:9606"
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1. .720
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177 c 159 g 198 t 1 othe
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/db_xref="taxon:40559"
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T4 cDNA library under conditions
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Human presenilin-2
Human presenilin-2
Human AD4 protein
Full AD4/AD3LP seq
Human AD4 gene gen
Rice glutelin-1 pr
Partial P. punctat
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Beta-2 adrenalin r
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RESOLT V5261LT V5261LT
                                                                                                                                                             V52614 standard; cDNA; 3451 BP.
V52614;
V52614;
V52614;
P1-DEC-1998 (first entry)
Human betta-2-adrenergic receptor cDNA.
Beta-2-adrenergic receptor; human; asthma; beta-agonist; polymorphism; ds.
Homo sapiens.
                                                                        variation
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N

Location/Qualifiers 1588. .2829 /*tag- a 1633 /*tag- b

/*tag- b
/note- *A to G substitution, results in
/note to Gly amino acid change*

.2 74.7 2452 74.7 4522 74.7 4542 74.7 5712 74.7 5712 74.7 5712 74.7 5712 74.7 5723 74.7 2738 72.6 548 72.6 548 72.6 548 72.6 548 72.6 548 72.6 548 72.6 549 (first erectant in subtication of the sease; ss.) .1 cdisease; ss1 coat4 tag4 tag4 tag4 tag4 tag4 tag5 in Joo4 tag6 3-A17 tag6 3-A17 tag8 1997; JOO9821996; JP-072914 .8 JP-072914 .9 JP-	•
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RESULT
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ID AC DOT DE SENT DE S
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11-SEP-1998; U03908.
26-FEB-1998; U03908.
03-MAR-1997; US-811441.
(BGHM ) BRIGHAM & WOMENS HO:
BOUSHEY H, Chinchilli VM, Di
Martin RJ;
WPI; 98-506372/43.
P-PSDB; W75777.
                                                                                                                                               27-MAR-1996; JP-072914.
(DAIN) DAINIPPON PHARM CO LTD.
FUJLI K, Furutani Y, Kawashima H,
WPI; 97-489627/45.
P-ESDB; W34319.
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Disclosure; Page 33-35; 46pp; English.
This cDNA sequence codes for human beta-2-adrenergic
W75777) having an arginine residue at position 16. A
for identifying individuals susceptible to adverse re
                                                                                                                                                                                                                                                                 WO9735963-A1.
02-OCT-1997.
24-MAR-1997; J
27-MAR-1996; J
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Novel beta-2 adrenalin receptor sub-type - useful for screening agonists and antagonists and researching asthmatic diseases claim 5; Page 23-26; 47pp; Japanese.
This sequence encodes the protein of the invention. The protein invention is a beta-2 adrenalin receptor subtype with Kd value approximately 75 pM against 1251-cyanopindrol. The protein can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta-2 adrenalin receptor Beta-2 adrenalin subtype;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthmatic disease; ss
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19; Conser
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                                                                                                                                                                                                                                                                                          J00982.
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/note= "Xaa=Leu, Ile"
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Pred. No.
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osition 16 of
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    useful for asthmatic dis

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     n of the of be used
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X3339L/r
X3339L/r
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ID X333
DT 333J
DT 30-J
DE PEBP
KW OSTEP
OST MUS
OS
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asthmatic
Sequence
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11-MAR-1999.
02-SEP-1998;
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x33329;
30-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases e.g. ostcoporosis

Example 15; Page 75-76; 118pp; Japanese.

The present invention describes DNA which participates in the regulation of expression of PEBP2 alpha A gene. The DNA produces a regulator protein with the activity of promoting bone formation and can serve as a promoter for prevention and treatment of bone diseases including osteoporosis. The present sequence represents a polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SUMU ) SUMITOMO PHARM CO LTD. Fujiwara M, Harada H, Katsumata Ogawa S, Tagashira S;
WPI: 99-243621/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-APR-1998; JP-114135.
02-SEP-1997; JP-254250.
15-OCT-1997; JP-299407.
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PEBP2 alpha
                                                                                                                                                                                                      14-OCT-1998 (first entry)
Canine beta-2 adrenergic re
Canine; beta-adrenergic re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA regulating expression of protein, useful as promoter
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                                                                                                                                                                                                                                              V30468;
14-OCT-1998
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              W09735973-A2.
02-OCT-1997.
26-MAR-1997; F00537.
26-MAR-1996; FR-003730.
                                                                                                                                                                    Canis
                                                                                                                                                                                                                                                                                     V30468
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                                                                                                                                                                                        hybridisation;
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(VETI-)
                                                                                                                                                                                                                                                                                                                                                                                 114 AACGCCAGAGCCTTCTTGC
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17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 BP;
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ds.
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                                                                                                                                                                                    ligand;
                                                                                      /product=
                                                                                                                                    169.
                                                                                                              /*tag=
                                                                                                                                                  ocation/Qualifiers
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94
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                                                                                                                                                                                                                              receptor
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                                                                                              "beta-2
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Pred. No. 37;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEBP2 alphaA gene to produce regulator for prevention or/and treatment of bone
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                                                                                              adrenergic receptor
                                                                                                                                                                                                              brown
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                                                                                                                                                                                                                tissue;
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                                                                                                                                                                                                              probe; human;
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pr factor Osf2 - useful for, e.g. treatment of osteogenic diseases, in pr vaccines and for diagnosis

PS Claim 5; Pages 185-187; 273pp; English.

CC This DNA encodes a native Osf2/Cbfal polypeptide (an osteoblast specific factor-2 encoded by the CBFAl locus). Host cells containing a vector comprising a Osf2/Cbfal nucleic acid are used for the recombinant CC production of the protein. The Osf2/Cbfal has osteoblast-specific comprising a Cilvity (particularly for treating osteogenic diseases, optionally when expressed from a gene therapy vector). Osf2/Cbfal is also cused to raise antibodies, to screen for modulators of its activity; used in vaccines and to detect specific antibodies (for diagnosis of bacterial CC infections). The Osf2/Cbfal polynucleotides can be used to produce transgenic animals or pluripotent non-human animal cells, while their fragments are used to detect Osf2/Cbfal genes by hybridisation, or as antisense molecules or ribozymes for downregulation of gene expression. CC Osf2/Cbfal polynucleotides are used for specific transcription of osteoblast-specific genes that have an OSE2 sequence element; to generate an immune response; in binding assavs to detect oser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PT Canine beta 2 and beta 3 adrenergic receptors and coding sequences - PT useful for identifying specific ligands and (ant)agonists to develop specific treatments for obesity in dogs

PS Claim 1; Page 45-46; 79pp; French.

CC receptor (RA-Ca-b2) gene. The sequence was isolated from a CDNA library CC constructed from polyA+ RNA purified from dog brown adipose tissue cells.

CC The probe was a 600 bp fragment of the coding region of the human beta-3 CC adrenergic receptor covering the region from the initiation codon to CC transmembrane domain 5 (TM5). The full length insert was cloned into M13 CC expressed e.g. in a mammalian cell, by subcloning into an expression CC expressed e.g. in a mammalian cell, by subcloning into an expression CC expressed e.g. in a mammalian cell, by subcloning into an expression CC expressed e.g. the beta-2 receptor can be used in comparative Structure-function studies, e.g. for differential screening of ligands CC specific for RA-Ca-b2 or RA-Ca-b3 (W44933).

SQ Sequence 2679 BP; 577 A; 736 C; 724 G; 642 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9f2/Cbfal polypetide encoding DNA.
O9f2/Cbfal; Osteoblast specific factor-2; CBFAl locus; transcriptional;
Osteogenic; gene therapy; modulator; bacterial infection; transgenic;
osteoblast; bone; osteocalcin; collagen; osteopontin; sialoprotein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid expressing the osteoblast-specific transcription factor Osf2 - useful for, e.g. treatment of osteogenic diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; W44932
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98-032136/03.
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17; Conservative
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/product= "Osf2/Cbfa1 polypeptide"
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105. .1895
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Pred. No. 44;
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RESULT
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PS Claim 72; Pages 155-156; 273pp; English.

CC Specific factor-2 encoded by the CBFA1 locus). Host cells containing a CC specific factor-2 encoded by the CBFA1 locus). Host cells containing a CC vector comprising a Osf2/Cbfa1 nucleic acid are used for the recombinant CC production of the protein. The Osf2/Cbfa1 has osteoblast-specific CC transcriptional activity (particularly for treating osteogenic diseases, CC optionally when expressed from a gene therapy vector). Osf2/Cbfa1 is also consider the containing of the service of the activity; used contained to detect specific antibodies (for diagnosis of bacterial infections). The Osf2/Cbfa1 polynucleotides can be used to produce transgenic animals or pluripotent non-human animal cells, while their cf ragments are used to detect Osf2/Cbfa1 genes by hybridisation, or as configuration of osteoblast-specific genes that have an OsE2 sequence cc element; to generate an immune response; in binding assays to detect OSE2 element; for purification of such elements and to induce differentiation of osteoblast progenitors for stimulating formation, growth, replacement can of osteoblast progenitors for stimulating formation, growth, replacement conficulty other genes to which Osf2/Cbfa1 can bind; for affinity other genes to which Osf2/Cbfa1 can bind; for affinity other genes to which Osf2/Cbfa1 can bind; for affinity other genes to which Osf2/Cbfa1 can bind; for affinity other genes to which Osf2/Cbfa1 can bind; for affinity other genes to which Osf2/Cbfa1 genes are used to genes, e.g. osteoblast-specific expression of homologous or heterologous contained contained benefic collagence and enhancer) from Osf2/Cbfa1 genes are used to collagence, and collagence and colla
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Best Local
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W09854322-A1.
03-DEC-1998; U10860.
29-MAY-1998; U2-080189.
24-MAR-1998; U3-080189.
29-MAY-1997; U3-048430.
(TEXA) UNIV TEXAS SYSTEM.
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Nucleic acid sequence of the Osf2 promoter and 5' UTR.

Osf2/Cbfal; osteoblast specific factor-2; CBFAl locus; transcriptional; osteogenic; gene therapy; modulator; bacterial infection; transgenic; osteogenic; osteocalcin; collagen; osteopontin; sialoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elements; for purification of such elements and to induce differentiation of osteoblast progenitors for stimulating formation, growth, replacement and repair of bone tissue. Antibodies, optionally, labelled, are used as immunoassay reagents for detecting Osf2/Cbfal; in DNA-binding assays to identify other genes to which Osf2/Cbfal and hid; for affinity purification of Osf2/Cbfal and to clone related genes. Also regulatory sequences (promoter and enhancer) from Osf2/Cbfal genes are used to provide osteoblast-specific expression of homologous or heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid expressing the osteoblast-specific transcription factor Osf2 - useful for, e.g. treatment of osteogenic diseases, vaccines and for diagnosis Claim 72; Pages 155-156; 273pp; English.
                    sialoprotein. The present sequence of the Osf2 promoter and 5' UTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ducy P, Karsenty G; WPI; 99-059837/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alternative splicing; ss.
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RESULT 9
V30458_4
Continuation (5 of 6) o
WP Sequence split into
WP Fragment Name
WP V30458_0
WP V30458_1
WP V30458_3
WP V30458_3
WP V30458_4
WP V30458_5
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02-SEP-1998; J03920.
08-APR-1998; JP-114135.
02-SEP-1997; JP-254250.
15-OCT-1997; JP-299407.
 96589
                                                                                                                                                                                                                                                                                                                                                 The present sequence represents DNA which participates in the regular of expression of PEBP2 alpha A gene. The DNA produces a regulator protein with the activity of promoting bone formation and can serve promoter for prevention and treatment of bone diseases including osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 aacggcagcgccttcttgc
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5851 AACGCCAGAGCCTTCTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                   DNA regulating expression of PEBP2 all protein, useful as promoter for preve diseases e.g. osteoporosis Claim 1; Page 76-85; 118pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUMU ) SUMITOMO PHARM CO LTD. FUjiwara M, Harada H, Katsumata Ogawa S, Tagashira S; WPI; 99-243621/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEBP2 alpha A gene expression regulating DNA sequence #4. PEBP2 alpha A gene; expression; regulation; bone disease; osteoporosis; ds.
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Sequence 1390
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17; Conser
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Pred. No. 4
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treatment of bone
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RESULT
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AC T45143;
OT 08-MAR-1997 (-
Flavobacterium ca
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V30459_4
Continuation (5 of 6) c
WP Sequence split into
WP Fragment Name
WP V30459_0
WP V30459_1
WP V30459_2
WP V30459_3
WP V30459_4
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(GEHO) GEN HOSPITAL CORP.
Binette F, Goetinck PF, T
WPL; 94-248890/30.
P-PSDB; R57350.
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                                                                                                                                                                                                                                                   promoting repair and attachment of cartilaginous tissue - using e.g. new fusion polypeptide of link protein and cartilage matrix protein, partic. for treating damage caused by arthritis Disclosure; Fig 5; 48pp; English.

The sequence shows the human cartilage link protein gene. The link protein can be used in conjunction with a cartilage matrix protein to promote binding of a complex of proteoplyvan and hyaluronic acid to collagen. The protein can be used to treat cartilage in joints esp. after damage by arthritis (esp. osteoarthritis) or to promote cartilage matrix formation in vitro to provide materiall for restorative or cosmetic surgery. It also promotes attachment to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cartilage link protein gene. CMP; proteoglycan; hyaluronic acid surgery; attachment; prostheses; i
                                                                                                                               1212
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Q70142;
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Sequence
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04-JAN-1994; U00253
06-JAN-1993; US-001
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378 A; 326 C;
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Pred. No. 60;
0; Mismatches
                                                                                                                                                                           Score 15.4; I
Pred. No. 65;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid; arthritis; osteoarthritis;
es; implants; tissue graft; LP; s
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210000
310000
410000
510000
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V30459
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                                                                                                                                                                                                 Length 1400;
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V30459
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standard;

DNA;

8625

ВP

(first entry)
um carotenoid

biosynthesis

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EP-747483-A2.
11-DEC-1996.
29-MAY-1996; 108556.
09-JUN-1995; EP-10888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carotenoid; lycopene; beta-carotene; echinenone; canthaxanthin; zeaxanthin; adonixonthin; astaxanthin; crtE; geranylgeranyl pyrophosphate synthase; GGPP synthase; crtB; prephytoene synthase; phytoene synthase; phytoene synthase; crtI; phytoene desaturase; crtY; lycopene cyclase; crtZ; beta-carotene hydroxylase; ds. Flavobacterium sp. R1534 WT (ATCC 21588).
               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cda
                               P-PSDB;
                                       P-PSDB;
                                              (HOFF) HOFFMANN LA ROCHE HOhmann H, Pagamontes L, WPI; 97-023160/03.
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Key
W06514;
W06515;
W06516;
W06516;
W00871;
W06517;
                                                                       EP-108888
                                                                                                                                                            /*tag= 1
/note= "base 8590 :
specification"
e 8592
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/note= "base 8581
specification"
e 8590
                                                                                                                            /note= "base 85
specification"
a 8602. .8604
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/note= "bases 8539-8540
specification"
8581
                                                                                                                                                                                                                                                         /note- "bases 8348-8349 specification" 8539. 8540
                                                                                                                                                                                                                                                                                   /label= ORF-16
8348. .8349
/*tag= 1
                                                                                                     /note= "bases 8602-8604 are specification"
                                                                                                                                                                                                                                                                                                                                                                                                             /product- (pre)phytoene synthase complement (4313. .5797)
                                                                                                                                                                                                                                                                                                                complement (7767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (3405. .4316)
                                                                                                                                                                                                                                                                                                                         /product-
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/label- Cryz
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1 aacggcagcgccttctt

Query Match Best Local S Matches 16

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81.1%; nilarity 94.1%; Conservative

B ;

Length 8991;

1:

0

Gaps

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infection.

PT infection.

PS Claim 1; Page 1239-1244; 2084pp; English.

CC A computer readable medium has been developed which has recorded on it CC 982 nucleotide sequences isolated from the Enterococcus faccalis genome. CC 12938 to X13919 represent these nucleotide sequences which are primary CC nucleotide sequences, also known as contigs. The computer-based system CC can identify fragments of the Enterococcus faecalis genome with CC commercial importance. The products can be used to detect the presence CC of Enterococcus faecalis in samples. They can also be used for CC diagnosing Enterococcal infection in an animal and monitoring CC progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or CC another related organism, in vivo or in vitro. In particular the constant of the property of the Enterococcus faecalis nucleotide sequences and the property of the Enterococcus faecalis nucleotide sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prelavobacterium gene sequences encoding carotenoid biosynthesis of enzymes - for the production of carotenoid(s), useful in foods and animal feeds
Tanimal feeds
Example 2; Fig 7; 80pp; English.
Sequence was deduced from the carotenoid biosynthesis pathway. The sequence was deduced from the carotenoid biosynthesis pathway. The sequence was deduced from inserts of 6 clones obtd. from genomic libraries e.g. by PCR amplification (see also T45144-45) and use of partial clones to screen the library. The identities of the gene products (see also W06513-19 and W00871) were detd. by examining carotenoid accumulation in E. coli hosts transformed with deleted variants of the gene cluster. The isolated genes can be used in different combinations to produce carotenoids in transformed host cells.
Sequence 8625 BP; 1458 A; 2898 C; 2964 G; 1295 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
WPI; 99-045171/04.
New isolated Enterococcus faecalis polynucleotides and polypeptides
- used to develop products for the detection of Enterococcus and for
use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecalis genome contig SEQ ID NO:258.
Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
Enterococcus faecalis.
MO9850555-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4503 ACGGCAGCGCCTTCTCG 4487
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P-PSDB; W06519.
                                                                                                Sequence
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                                                                                                                   Infection.
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Pred. No. 77;
0; Mismatches
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Pred. No. 76;
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В

8630 AATGGCAGCGCCTTCTT

8646

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RESULT 14
T87401/c
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                             W09634099-A2.
31-OCT-1996; CA0263.
29-APR-1996; US-431048.
28-APR-1995; US-431048.
R 28-JUN-1995; US-496841.
R 31-JUL-1995; US-509359.
A (HSCR-) HSC REES & DEV LP.
A (UTOR) UNIV TORONTO GOVERNING COUNCIL.
OTOR OF ROMMENS JM, St George-Hyslog
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identifying genes which cause chromosome missegregation - useful for identifying genes of and treatments for diseases, e.g. Alzheimer's disease, cancer and ageing claim 16; Fig 1; 77pp; English.

Identifying genes which cause improper chromosome segregation, identifying genes which cause improper chromosome segregation and processes caused by genes encoding chromosome missegregation promoters was exemplified using Alzheimer's disease. The sequences given in T87401 to T87426 can be used in the above methods. It is not clear from the figure legend, the figure and the disclosure of the specification which sequence of Fig 1 and Fig 28 is the AD4/AD3LP or the AD3 sequence.

Sequence 1417 BP; 307 A; 385 C; 380 G; 345 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9707213-A2.
27-FEB-1997.
15-AUG-1996; U
16-AUG-1995; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T87401;
07-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HARD ) HARVARD COLLEGE.
Li J, Potter H;
WPI; 97-165297/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        presentlin; inhibitor; AD;
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                                                                                                                                                                                                                                                                                                                                                                              1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AD3; AD4/AD3LP;
                                                                                                                                                                                                                             Human presentiin-2 wild type coding sequence.

Human presentiin-2; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; familial Alzheimer's disease; cerebral haemorrhage; schizophrenia; depression; antibody; gene expression modulator; therapy; ss.
                                                                                                                                                                                                                                                                                   T40031;
25-JUL-1997 (first entry)
         Fraser PE, Rommens WPI; 96-497631/49. P-PSDB; W05762.
                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                             T40031 standard; DNA; 2229
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presentlin genes - useful for diagnosis, therapy
                                                                                                                                                                                                                                                                                                                                                                                GGCAGCGCCTTCTTG 1033
                                                                                                                                                                                                                                                                                                                                                                                          ggcagcgccttcttg 18
                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease; chromosome; missegregation; ibitor; AD; trisomy 21; ss.
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/product=
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                                                                                                                                                                       Location/Qualifiers
366. 1712
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.9%;
                                                                                                                                                               presenilin-2
                                                                                                                                                                                                                                                                                                                BP.
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                                       George-Hyslop
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Pred. No.
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J. 1e+02;
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     and drug
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pr screening of familial Alzheimer's disease, cerebral disorders, etc. ps Claim 8; page 148-150; 178pp; English.

CC This sequence represents the coding sequence for the human presenilin-2. This sequence represent the coding sequences for the two different cryonoms of wild type human presentilin-1 (PS-1). The form represented by CC T40029 results from alternate splicing of the genomic DNA sequence. CC T40029 resents the coding sequence for wild type mouse PS-1. The CC presentilins are a family of highly conserved integral membrane proteins common mutational hot spot regions. Mutations in PS genes are implicated common mutational hot spot regions. Mutations in PS genes are implicated common mutational hot spot regions. Mutations in PS genes are implicated common mutational hot spot regions. Mutations in PS genes are implicated common mutational hot spot regions. Mutations in PS genes are implicated common familial Alzheimer's disease (AD) and possibly other diseases such as CC cerebral haemorrhage, schizophrenia, depression etc. So detection of containing containing containing contains sequences antibodies selective for mutant forms of the encoded proteins (such as W05736) and modulators of PS gene expression are useful potentially useful for treatment of AD etc. Transgenic animals are useful caffinity purification and in-immunoassays.

SQ Sequence 2229 BP; 481 A; 579 C; 633 G; 521 T;
В
                                        20
                                                                                           Matches
                                                                                                                  Query Match
Best Local :
1606 GGCAGCGCCTTCTTG
                            4 ggcagcgccttcttg
                                                                                              15;
                                                                                                                  Similarity
                                                                                           Conservative
                                                                                                                     78.9%;
  1592
                                                18
                                                                                                0,
                                                                                                                       Score 15;
Pred. No.
                                                                                                   Mismatches
                                                                                                                       DB 1; Lo
1.1e+02;
                                                                                                     0;
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Perfect score:
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1: /cgn2_6/ptodata/1

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US-08-001-078A-2
US-08-463-218-2
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Sequence 3, Sequence 2, Sequence 2, Sequence 18, Sequence 18, Sequence 163, Sequence 1, Se
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1,	Sequence 12, Appl	Sequence 12, Appl	Sequence 2, Appli	Sequence 3, Appli	Sequence 1, Appl1	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appl1	Sequence 1, Appli	Sequence 2, Appl1	Sequence 19, Appl	Sequence 19, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 1, Appl1	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

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; NAME/KEY:
; LOCATION:
PCT-US91-00909-3
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:

AMAE: MBK1, DAV1d J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 99000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

TELEFAX: 206-622-6031

TELEFAX: 3723836

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENCTH: 1242 base pairs
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GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Methods of Producing Hybrid G
TITLE OF INVENTION: Protein-Coupled Receptors
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Ave.
                                                                                  STRANDEDNESS: Since TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: POFILING DATE: 19910208
CLASSIFICATION: 435
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STATE: Washington
COUNTRY: United S
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US-08-463-218-2/c
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Best Local Similarity
Matches 16; Conserv
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Patent No. 5872094
                                                                                                                                                                          Sequence 2, Application US/08463218 Patent No. 5986052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MYOTS, PAUL L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,07
FILLING DATE: 06-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tondravi, M., Mehrdad APPLICANT: Binette, Francois TITLE OF INVENTION: METHODS FOR ITITLE OF INVENTION: FORMATION UNMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                 APPLICANT: Goetinck, Paul F.
APPLICANT: Tondravi, Mehrdad
APPLICANT: Binette, Francois
TITLE OF INVENTION: METHODS:
TITLE OF INVENTION: FORMATIO
                                                                                                                                                                                                                                                                                    1212 ACTGCAGCGCCTTCTTG 1196
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LENGTH: 1400 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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60 STATE STREET, Suite 510
60 STATE STREET, Suite 510
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                  LAHIVE & COCKFIELD
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                                                                     Francois
METHODS FOR PROMOTING CARTILAGE MATRIX
FORMATION
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94.1%;
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PCT-US94-00253-2/c

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                                                                                                                         ; TOPOLOGY: PCT-US94-00253-2
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Best Local :
                                                         Query Match
Best Local
                                          Matches
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EFILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,078
EFILING DATE: 06-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-008DV
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 06-JAN-1993 INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                            COMPUTER: IBM PC compat
OPERATING SYSTEM: PC-DO
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 227-59.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1212 ACTGCAGCGCCTTCTTG 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: ASCII text CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                     LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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2 acggcagcgccttcttg 18
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                                            Conservative
                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                            81.1%;
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                                                            Score 15.4;
Pred. No. 42;
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Pred. No. 4
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                                               Mismatches
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RESULT 6
US-08-888-077A-18/c
: Sequence 18, Application US/08888077A
: Patent No. 6020143
: Patent No. 6020143
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Best Local S
Matches 15
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                                                                                                                GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROWENS, JOHANNA M
APPLICANT: FRASER, PAUL E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (781) 861-9540 INFORMATION FOR SEQ ID NO: 1:
                              TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFO CUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                1047 GCCAGCGCCTTCTTG 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Granahan Esq., Patricia
REGISTRATION NUMBER: 32,727
REFERENCE/DOCKET NUMBER: HU95-03PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,448
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Granahan Esq., Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1417 base pairs
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Massachusetts
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                    DDRESSEE:
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ELERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK 600 SOUTH AVENUE WEST
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ENTION: ASSAY FOR IDENTIFYING GENES CAUSING
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..2226
; OTHER INFORMATION: /note= "hPS2"
US-08-888-077A-18
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                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   APPLICANT: Huntington Potter and Jinhue Li
TITLE OF INVENTION: ASSAY FOR IDENTIFYING GENES CAUSING
TITLE OF INVENTION: CHROMOSOME NON-DISJUNCTION
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1606 GGCAGCGCCTTCTTG 1592
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REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 654-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/592,541 FILING DATE: 26-JAN-1996 ATTORNEY/AGENT INFORMATION: NAME: PALISI, THOMAS M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2229 base pair
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                               STREET: Two Militia I CITY: Lexington STATE: Massachusetts
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LOCATION:
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                              APPLICATION NUMBER: FILING DATE: 08-AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 03-JUL-1997 CLASSIFICATION: 530
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STATE: NJ
                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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US/08/875,972

08-AUG-97

ON: 435
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FILING DATE: 16-AUG-1995 ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 6 FILING DATE: 16-AUG-1995

US 60/002,448

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; MOLECULE TYPE: DNA (genomic) US-08-875-972-28
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                              TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2285 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (781) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES
TITLE OF INVENTION: TO ALZHEIMER'S DIS
                                                                                                                                         ATTORNEY/AGENY INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1648 GGCAGCGCCTTCTTG 1634
                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Granahan Esq., Patricia REGISTRATION NUMBER: 32,227 REFERENCE/DOCKET NUMBER: HU95-TELECOMMUNICATION INFORMATION: TELEPHONE: (781) 861-6240
MOLECULE TYPE:
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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LENGTH: 2276 base pairs
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 10-NOT CLASSIFICATION: 43
                                                  TYPE: nucleic acid
                  TOPOLOGY:
                                 STRANDEDNESS:
                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
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10-NOV-1997
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                               single
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                                                                                                           136:
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RESULT 10
US-08-651-136C-63
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                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 136:
                                                                                               Sequence 63, Application US/08651136C Patent No. 6001639 GENERAL INFORMATION:
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 15; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 136,
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Best Local
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                                                     APPLICANT:
APPLICANT:
             APPLICANT:
APPLICANT:
                                                                                                                                                                                                  1606 GGCAGCGCCTTCTTG 1592
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1606 GGCAGCGCCTTCTTG 1592
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ST. GEORGE-HYSLOP,
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: sintopology: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/592,541 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: High
CITY: Boston
                                                                                                                                                                                                                4 ggcagcgccttcttg 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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15; Conservative
                                                                                                                                                                                                                                                                                                                                                                 : 2285 base pairs
nucleic acid
EDNESS: single
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High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08592541
                                                                                                                                                                                                                                                         Conservative
                                                    Andersen, Lene N.
Lassen, Soren F.
                         Kauppinen, Markus
Lange, Lene
Ihara, Michiko
              Nielsen,
                                                                                Schulein, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEORGE-HYSLOP, PETER
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                                                                                                                                                                                                                                                                     78.9%;
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100.0%; Pred. No.
tive 0; Mismatcl
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                                                                                                                                                                                                                                                                       Score 15;
Pred. No.
                                                                                                                                                                                                                                                         Mismatches
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66;
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                                                                                                                                                                                                                                                                                    Length 2285;
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Best Local Similarity 93.8
                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08270013B Patent No. 5686294 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-867-01:
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/270,013B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,136C
FILING DATE: 21-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                           APPLICANT: Sogabe et al.
TITLE OF INVENTION: PROTEIN HAVING HEAT-RES
TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
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APPLICATION NUMBER: US/0 FILING DATE: 01-JUL-1994 CLASSIFICATION: 435
                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                              STREET: Two PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 CGGCAGCGCCTTCATG 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 2...
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                                                                                                                                                            RY: USA
61601-6780
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                                                                                                                                                                                               Illinois
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93.8%;
                                                                                                                                                                                                                                                                                                      PROTEIN HAVING HEAT-RESISTANT MALATE DEHYDROGENASE ACTIVITY
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: (25)3533
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1912 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 15; Conserv
            APPLICATION NUMBER: US 08/270,013
FILING DATE: 01-70L-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 164701/1993
FILING DATE: 02-70L-1993
ATTORNEY/AGENT INFORMATION:
NAME: HOOVET, Allen E.
REGISTRATION NUMBER: 37354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: COMPATIBLE
COMPUTER: PM COMPATIBLE
COMPUTER: PM COMPATIBLE
COMPUTER: PATENTIAN RELEASE #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1361 AACGGCAGCGCCTACT 1376
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ORGANISM: Bacillus stearothermophilus
STRAIN: ATCC12016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sogabe et al.
TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE
TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
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ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                           APPLICATION NUMBER: US/08/838,418 FILING DATE: 17-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Pa
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 2
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPOLOGY:
                                                                                                                                                                                                                                                                                                                                                       60601-6780
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                                                                                                                                                                                                                                                                                                                                                                                    Illinois
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93.8%;
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Pred. No. 1
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TELEX: (25)3533
INFORMATION FOR SEQ'ID NO:

TELEFAX:

(312) 616-5700

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RESULT 13
US-08-220-240A-4
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Best Local S
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Patent No. 5955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: Bacillus stearothermophilus
STRAIN: ATCC12016
               TELEFAX: (312) 474-0448 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1361 AACGGCAGCGCCTACT 1376
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0
FILING DATE: 29-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ANTIBODIES RECOGNIZING TIE RECEPTOR TITLE OF INVENTION: TYROSINE KINASE AND USES THEREOF NUMBER OF SEQUENCES: 5
                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 09-JAN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                             REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474,6300
                                                                                                                                                                                                                                 FILING DATE: 08-JAN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
SEQUENCE CHARACTERISTICS:
                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                               APPLICATION NUMBER: US 08/167,453 FILING DATE: 15-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                RY: Unites States of America 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08220240A
                                                                                                                Gass,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Illinois
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Partanen, Juha
Makela, Tomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 South Wacker Drive/6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Korhonen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                         David A.
David R.
38,153
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93.8%;
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Pred. No. 1.3e+02;
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            Query Match
Best Local Similarity
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Matches
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NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                   TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/384,106A FILING DATE: 06-FEB-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: InK4C-p18 and InK4d-p19, Inhibitors of TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                FEATURE:
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Local Similarity 93.8%;
nes 15; Conservativo
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                  NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                              TOPOLOGY:
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Hirai Ph.D.,
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 Conservative
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84.2%;
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Pred. No. 1.3e-
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               Score 14.2; DB 5;
pred. No. 1.4e+02;
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                                Length 501;
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PCT-US96-01643-8/c
; Sequence 8, Application PC/TUS9601643
; GENERAL IMPORMATION:
; APPLICANT: St. Jude Children's Research Hospital
; TITLE OF INVENTION: INK4C-pl8 and INK4d-Pl9, Inhibitors of
TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KSSSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                     FEATURE:

NAME/KEY:

LOCATION:

PCT-US96-01643-8
Search completed: September 12, 2000, 23:04:32 Job time: 3939 sec
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                                                                                               В
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ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAMUEL L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SED ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local S
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US96/01643
FILING DATE: 06-FEB-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/384,106
FILING DATE: 06-FEB-1995
                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: p19
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
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143 ACCTGCAGCGCCGTCTTGC 125
                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington STATE: D.C.
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84.2%; Pred. No. 1.4e+02;
Live 0; Mismatches 3
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Minimum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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58: em_est20:
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Result No.

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SUMMARIES

AI475044 AW139725 C18250

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AI128872 qf16g08.s
AI199676 qi60a09.x
AI198151 wk32f10.x
AI2981616 tm62e03.x
AA234907 zs38f03.r
AA150236 z103c01.r
N27820 yx54h10.r1
R86608 RABEST229T
AI413640 mb29h12.x
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AUTHORS
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                                                                                                                                                                                                                                                National Cancer Institute / National Disorders and Stroke, Brain Tumor Gen (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACGGCAGCGCCTTCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
             CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1052 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                  NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
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19; Conserv
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Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
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Kyushiki, H., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimar
Shinomiya, H., Suzuki, M., Takaichi, A., Takeda, S., Watanabe, T.,
Maekawa, H., Nakamura, Y. and Takahashi, E.
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Tel: 0886-65-2888
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/clone_lib="Human placenta cDNA (TFujiwara)"
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113 c 101 g
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/db_xref="taxon:9606"
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clone IMAGE:2162716
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Shimada,Y.,
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C18250 377 bp mRN
C18250 Human placenta cDNA
GEN-559E06 5', mRNA sequenc
   mRNA sequence.
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                 sapiens cDNA clone
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AI836000 AQ803246 AW533116 AW186808

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AI844706 AI390851 AW046979

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UI-H-BII-aeb-b-10-0-UI.s1 NCI_CGAP_Sub3
IMAGE:2718667 3', mRNA sequence.
ANJ39725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov_bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
On Jun 22, 1998 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/ob_xref="taxon:9606"
/clone="IMAGE:2718667"
/clone=lib="NCI_CGAP_Sub3"
/lab_host="DH10B (Life Technologies)"
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/clone="IMAGE:2162716"
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Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                           Unpublished (1998)
On May 18, 1998 this sequence version Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                     1 (bases 1 to 369)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                       AI128872 369 bp mRNA EST 13-FEB-1999 qf16g08.sl NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750238 mRNA sequence.
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AI128872.1 GI:3597386
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                     Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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                                                                                                           cDNA Library Preparation: M. Bento Soares, Ph.D.,
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                                                                                                                                                     Robert_Strausberg@nih.gov
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Pred. No. 1.1e+02;
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                                                     Sequencing Center information can be
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RESULT
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 442)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGAP), Tumor Gene Index
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Location/Qualifiers
                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 959 Std Error: 0.00
                                                                                                                                                                                                                                        cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: M. Bento Soares, Ph.D., Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1998)
On Oct 6, 1998 this sequence version replaced gi:3709712.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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AI199676
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/clone="TMAGE:1860856"
/clone_lib="NCI_CGAP_Brn25"
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/lab_host="DH10B"
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/lab_host="DH10B"
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/clone="IMAGE:1750238"
/clone_lib="NCI_CGAP_Brn25"
                                                                                                  /organism="Homo sapiens"
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Pred. No. 1.1e+02;
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18; Conserv
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Tel: (301) 496_1550
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                Seq primer: -40UP from Gibco
High quality sequence stop: 4
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                  quality sequence stop: 440.
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Procurement: David N. Lou
adaptors (Pharmacia), digested with Not I at the Not I and Eco RI sites of the modified Library is normalized, and was constructed
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192 c 138 g 58 t
                                                                                                                                                  /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH108"
                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2414059"
/clone_lib="NCI_CGAP_Brn25"
                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1998)
On Oct 13, 1998 this sequence version replaced gi:3738881.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
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tm62e03.x5 NCI_CGAP_Brn25 Hor
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Tissue Procurement: David N. Lou
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
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         /clone="IMAGE:2162716"
/clone_11b="NCI_CGAP_Brn25"
/tlssue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                             /db_xref-"taxon:
                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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94.7%;
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Pred. No. 1.1e
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information
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IMAGE:2162716 3';
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar to
AA234907
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zs38f03.rl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 422)
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           88
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/note-*Organ: mixed (see below); Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHHJ9W) were mixed, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 360232-265223, 340488-345479, and 484488-489479.*
                                                                                                                                                                                                                                                                                                 /tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:687485"
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:5591635"
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                                                                                                                                                                                                                                                                          'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares_NhHMPu_S1"
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Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:687485 5'
TR:G1213518 G1213518 ALG3 ;, mRNA sequence.
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Best Local Query Match

l Similarity 16; Conserv

Conservative

100.08; **

Score 16; DB; ; Pred. No. 5.2, 0; Mismatches

DB 23; 5.2e+02

Length 422; Indels

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Matches

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AA150236/c
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 CGGCAGCGCCTTCTTG 112
                               cggcagcgccttcttg 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Dietrich, N., Kucaba, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Mardis, E., Moore, B., Morris, M., Parsons, J., Frange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 825 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia;
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                                                                                    Similarity
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h quality sequence stop: 401.
                                                                                                                                                                             82
                                                                      Conservative
                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:3805819"
/db_xref="taxon:9606"
/clone="IMAGE:491232"
                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
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vay, Box 8501, St. Louis,
                                                                                        Score 16;
Pred. No.
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1 (bases 1 to 498)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N27820 498 bp mRNA EST 30-DEC-1:
yx54h10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:265603 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stops: 220
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on Oct 18, 1995 this sequence version replaced g1:1023122
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The WashU-Merck EST Project
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
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   R86608
R86608.1
                                                                                                                                                                                                                                  l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                       R86608 195 bp mRNA EST 17-AUG-1995 RABEST229T RABEST229T RABEST229 5' similar to cofilin, mRNA sequence.
                                   cDNA clone pRABOC229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop: 220.
Location/Qualifiers
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                             99
                                                                                                                                                                                                                                                                                                                                         double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTTT3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino." 125 c 137 g 131 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:265603"
/clone_lib="Soares melanocyte 2NbHM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:3875245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex-"Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
     GI:947286
                                                                                                                                                                                                                                                       84.2%;
100.0%;
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                                                                                                                                                                                                                                                         Score 16;
Pred. No.
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                                                                                                                                                                                                                                        DB 86; I
5.3e+02;
hes 0;
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AUTHORS
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AI413640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACAGCACCGCCTTCTTGC
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                               AI413640 197 bp mRNA EST mb29h12.x1 Soares mouse p3NWF19.5 Mus musculus IMAGE:330887 3', mRNA sequence.
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Sakal, D., Tong, H. S. and Minkin, C.
Ostcoclast Molecular Phenotyping by Random cDNA Sequencing
Bone 17 (2), 111-119 (1995)
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USC School of Dentistry, 925 West 34th
Angeles, CA 90089-0641
Tel: 2137405563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 2137407560
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Seg primer: T7 promoter
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//db_xref="taxon:9986"
//clone="pRABOC229"
//clone_lib="Rabbit Ostcoclast, Dennis Sakai"
//lab_host="E. coli DH125"
//note="vector: pSPORT1; Site_1: Sali; Site_2: NotI;
/note="vector: pSPORT1; Site_1: Sali; Site_2: NotI;
/note="vector: pSPORT1; Site_1: Sali; Site_2: NotI;
/note="vector: pSPORT1; Site_1: Sali; Sali; Sali; Sali; Sali;
/note="vector: pSPORT1; Site_1: Sali; S
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89.5%;
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Pred. No. 5.2e+02;
0; Mismatches 2;
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R86588/c
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          University of Southern California
USC School of Dentistry, 925 West 34th Street,
Angeles, CA 90089-0641
Tel: 2137405563
Teax: 2137407560
                                                                                                                             Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

1 (bases 1 to 234)
Sakai,D., Tong,H.-S. and Minkin,C.
Osteoclast Molecular Phenotyping by Random cDNA Sequencing Bone 17 (2), 111-119 (1995)
90021365
On May 10, 1995 this sequence version replaced gi:805875.
Other_ESTs: RABEST038T, RABEST045T, RABEST103T, RABEST140T, RABEST202T, RABEST229T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4444 Forest Park Parkway, Box 8501, Tel: 314 286 1800 Fax: 314 286 1810
                                                                                              Contact: Sakai D
Basic Sciences
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RABEST163T Rabbit Osteoclast, Dennis Sakai Oryctolagus cunicu
CDNA clone pRABOC163 5' similar to cofilin, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty/free through LLNL; contact the
IMAGE Consortium (info@inage.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashJ-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashJ-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                     EST.
Oryctolagus cuniculus.
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sakai@molbio.usc.edu
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/db_xref="taxon:10090"
/clone="IMAGE:330887"
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89.5%;
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RABEST140T Rabbit Osteoclast, Dennis Sakai Oryctolagus cuniculus
cDNA clone pRABOC140 5' similar to cofilin, mRNA sequence.
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Seq primer: T7 promoter
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Sakai,D., Tong,H.-S. and Minkin,C.
Osteoclast Molecular Phenotyping by Random cDNA Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus. Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                       On Jan 5, 1998 this sequence version replaced gi:1269099. Other ESTs: RABEST038T, RABEST045T, RABEST084T, RABEST103T, RABEST163T, RABEST202T, RABEST229T Contact: Sakai D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R86566.1 GI:947220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA clone pRABOC140
                                                                                                                                                                                                                                                                                                      University of Southern California
USC School of Dentistry, 925 West
Angeles, CA 90089-0641
Tel: 2137405563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                          Insert Length: 629 Sto
Seg primer: T7 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bone 17 (2), 111-119 (1995)
                                                                                                                                                                                 High quality sequence stop: 233.
                                                                                                                                                                                                                                                                                                                                                                                                         Basic Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Rabbit Osteoclast, Dennis Sakai"
/clone_lib="Rabbit Osteoclast, Dennis Sakai"
/lab_host="E. coli DH125"
/note="Vector: pSpORT1; Site_1: Sal1; Site_2: Not1;
/note="Vector: pSpORT1; Site_1: Sal1; Site_2: Not1;
/note="Vector: pSpORT1; Site_1: Sal1; Site_2: Not1;
/note="Vector: pSpORT1; Site_1: Sal1; Site_2: Not1
osteoclasts prepared from the long bones of 10 day old
rabbits. First strand cDNA was synthesized by priming
with an oligo(dT)-Not1 anchor-primer and second strand
with an oligo(dT)-Not1 anchor-primer and second strand
cDNA was synthesized by replacement synthesis as described
by Gubler and Hoffman (Gene 25:283, 1983). Following the
addition of Sal1 adapters and Not1 digestion, the cDNA was
cloned between the Sal1 (50) and Not1 (30) sites of the
pSPORT1 (BRL) plasmid vector."

57 a 62 c 81 g 34 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                            sakai@molbio.usc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="New Zealand Words."
/db_xref="taxon:9986"
/clone="pRABOC163"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryctolagus cuniculus"
/strain="New Zealand White"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
                                                                  /strain="New Zealand White"
/db_xref="taxon:9986"
                                                                                                                                                              Location/Qualifiers
/clone_lib="Rabbit Osteoclast, Dennis Sakai"
/lab_host="E. coli DH12S"
                                            /clone="pRABOC140"
                                                                                                                    /organism="Oryctolagus cuniculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                     Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.8; DB 89;
Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                            925 West 34th Street, DEN-4220, Los
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.00
                                                                                                                                                                                                                                        0.00
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BASE COUNT
ORIGIN
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AUTHORS
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R86542/c
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KEYWORDS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 aacggcagcgccttcttgc 19
||| ||| ||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACAGCACCGCCTTCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RABESTIO3T Rabbit Oste cDNA clone pRABOC103 5 R86542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

1 (bases 1 to 275)
Sakai, D., Tong, H.-S. and Minkin, C.
Osteoclast Molecular Phenotyping by Random cDNA Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bone 17 (2), 111-119 (1995) 96021365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Jan 5, 1998 this sequence version replaced gi:1269075. Other ESTs: RABEST038T, RABEST045T, RABEST084T, RABEST140T, RABEST163T, RABEST202T, RABEST229T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R86542.1 GI:947196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: sakai@molbio.usc.edu
Insert Length: 737 Std Er:
Seq primer: T7 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Southern California
USC School of Dentistry, 925 West 34th Street, DEN-4220, Los
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Sakai D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angeles, CA 90089-0641
Tel: 2137405563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Basic Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 281.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2137407560
/clone_lib="Rabbit Ostooclast, Dennis Sakai"
//lab_host="E. coll DH12S"
//lab_host="E. coll DH2S"
//lab_host="E. coll DH12S"
//la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA was synthesized by replacement synthesis as described by Gubler and Hoffman (Gene 25:283, 1983). Following the addition of SalI adapters and NotI digestion, the cDNA was cloned between the SalI (50) and NotI (30) sites of the psporTI (BRL) plasmid vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: psport1; Site_1: Sall; Site_2: Not1; poly(A)+ RNA was purified from a 97% pure population of osteoclasts prepared from the long bones of 10 day old rabbits. First strand cDNA was synthesized by priming with an oligo(dr)-Not1 anchor-primer and second strand with an oligo(dr)-Not2 anchor-primer and second strand with anchor-primer and second strand with a second strand with a seco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="New Zealand |
/db_xref="taxon:9986"
/clone="pRABOC103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryctolagus cuniculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             White"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 opulation of
10 day old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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BASE COUNT

67

QV

В

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Outry Match
B3.28: Score 15.8: DB 89: Length 275;
Best Local Similarity 89.58: Pred. No. 6.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 anggongegotitctigg 19
Db 39 AACACCCCCCTTTTGC 21

Search completed: September 12, 2000, 22:46:44

Job time: 3786 sec
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OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 1000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
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    September 12, 2000, 23:02:47; Search time 930.45 Seconds (without alignments) 36.444 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Green, S.A., Turki, J., Innis, M. and Liggett, S.B.
Amino-terminal polymorphisms of the human beta 2-adrenergic
receptor impart distinct agonist-promoted regulatory propert
receptor impart distinct agonist-promoted regulatory propert
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1 (bases 1 to 1242)

Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B.
Mutations in the gene encoding for the beta 2-adrenergic rece; in normal and asthmatic subjects in normal and asthmatic subjects in promatic subjects in subjects in promatic sub
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1 (bases 1 to 1242)

Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B. Mutations in the gene encoding for the beta 2-adrenergic receptor in normal and asthmatic subjects
in normal and asthmatic subjects
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Green, S.A., Turki, J., Innis, M. and Liggett, S.B.
Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory proper blockemistry 33 (32), 9414-9419 (1994)
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Liggett, S.B. and Green, S.A.
Direct Submission
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1242)
Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B.
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Ave ML670564, Cincinnati, OH 45267-0564, USA
Location/Qualifiers
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Liggett,S.B. and Green,S.A.
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1 (bases 1 to 1286)
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Beta-2-adrenergic receptor allele frequencies in
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TVPSDNIDSQGRNCSTNDSLL"
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/chromosome="5"
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Rupert,J.R. and Hochachka,P.W.
Beta-2-adrenergic receptor allele frequencies in two native
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Homo sapiens beta-2-adrenergic
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6270 University Blvd., Vancouver,
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Rupert, J.R. and Hochachka, P.W.
Direct Submission
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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heterozygous for a known C/T mutation"
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IIMGTFTLCWLPFFIVNIVHYIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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349 c 3
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/chromosome="5"
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AF203386.1 G
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Submitted (09-NOV-1999) Zoology, Use Control (19-NOV-1999) Zoology, 
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1290)
Rupert, J.L. and Hochachka, P.W.
Beta 2 adrenergic receptor allele frequencies in two
                                                                                                                                                                                         complete cds.
U73206
U73206.1 GI:1657819
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19; Conser
                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutherla; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 1298)
                                                                                                                        Canis familiaris
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                      Huang, R.R., Rapoport, D., Schaeffer, M.T.,
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YSRVFOEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHCLRRSSKECLKEHKALKTLG
IIMGTFTLCWLPFFIVNIVHYJQDNLIRKEVVILLNWJGYVNSGENPLIYCRSDERI
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26. .12
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/db_xref="GI:6636496"
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26. .1267
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/db_xref="taxon:9606"
/chromosome="5"
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mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huang, R.
                                                                                                                                                                                                                                                                                                                                                                                                            Macaca.
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Amend, A.M. and Guan, X.M.
Cloning, sequencing, and expression of adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MACBZAR 1320 bp mRNA PRI 02-OCT-1995 Macaca mulatta beta-2 adrenergic receptor (B2AR) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular cloning
J. Recept. Signal
97364078
                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L38905.1 GI:1004338
beta-2 adrenergic receptor.
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                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca mulatta cDNA to mRNA.
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ang,R.-R.C., Rapoport,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="beta2 adrenergic receptor"
/product="beta2 adrenergic receptor"
/protein_id="AAB93647.1"
/db_xref="gi:1657820"
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NFWCEFWTSIDVLCVTASIETLCVIAVDRYFAITSFKYQSLLTKNKARVVILMVMIV
SGLTSSFLPIOMHWYRATHGEAINCYAKETCCDFFTNQAYAIASSIVSFYLPLVVMVFV
YSRVFQVAQROLQKIDRSEGRFHAQNLSQVEQDGRSGHGHRRSKFCLKEHKALKTLG
IIMGTFTLCWILPFIVNIVHVIQDNLIPKEVYILLNWVGYVNSAFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSNNSNSRSDYAGEHSGCHLGQEKDSELLCEDPPGTEDR
QGTVPSDSVDSQGRNCSTNDSLL"
60 a 396 c 359 g 283 t
                                                                                                                                                                                                                                                                Biol. 14 (9),
                                                                                                          /note="genomic DNA for this receptor sequenced
to be identical with the cDNA"
                                                                                                                                                   /organ1sm="Macaca mulatta"
/db_xref="taxon:9544".
                                                                                                                                                                                                                    Location/Qualifiers
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/db_xref="taxon:9615"
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/gene="B2AR"
1. .1320
                                                            /gene="B2AR"
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Felis catus |
AF192345
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19; Conserv
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Cully,D.F., Tremm1,G. and Zachwieja,S.
Direct Submission
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Eukaryota; l
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Cully, D.F., Tremml, G.
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2 (bases 1
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Eutheria; Carniyora; Fissipedia; Felidae; Felis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (05-OCT-1999) MRL, Merck & Co.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Felis domesticus beta
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larity 100.0%;
Conservative
/product="beta-2 adrenergic receptor"
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SGLTSELPIQMHWYRATHQEALNCYAKETCCDFTNQAYAIASSIVSFYLDLVVMVFV
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IIMGTFTLCMLPFTYMIVHVIQDNLLFKEVYILLMWVGYVNSAENPLIYCRSPDERI
AFQELLCLRRSSLKAYGNGYSNNSNSRTDYAGEHSGGPLGQEKDSEVLCEDPPGTENL
ANRQCTVPNDSIDSQCGNGSTNUSLL"

AURGCTVPNDSIDSGCGNGSTNUSLL"

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/product="beta-2 adrenergic receptor"
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/db_xref="GI:1004339"
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/translation="McGPGNGSAFILAPNGSHAPDHDVTQERDEAWVVGMGIVMSTFG
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LAIVFGNVLVITASIETLCVIAVDRYFAITSPFXYQSLLTKNKARVIILMKMWTV
SGLTSFIDIQMHWYRATHQEAINCYAKETCCDFFTNQAYAIASSIVSEYVPLUIVMVFV
SGLTSFIDIQMHWYRATHQEAINCYAKETCCDFFTNQAYAIASSIVSEYVPLUIVMVFV
YSRVFQDEAKROLOKINKSGRFHAQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
IIMGTFTLCWLPFFIVNIVHVIQDNLIPKEVYILLMWVGYVNSGFNPLIYCRSPDFRI
INGCTFTLCWLPFFIVNIVHVIQDNLIPKEVYILLMWVGYVNSGFNPLIYCRSPDFRI
INGCTFTLCWLPFFIVNIVHVIQDNLIPKEVYILLMWVGYVNSGFNPLIYCRSPDFVGH
ARQELLCLRRSSLKACCNGVSSNSNNTGEQSGTHLEQEKENKLLCEDLPGTEDFVGH
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1289. .1320
/gene="B2AR"
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41. .1288
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                                                                                                                                                                                                                                                                                                                                                               /note="synonym: Felis domesticus"
<6. .>1262
                                                                                                                                                                                                                                                                           receptor subtype
                                                                                                                                                                                                                                                                                                                                    /product="beta-2 adrenergic receptor"
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Felis catus"
/db_xref="taxon:9685"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                   /note="G-protein
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beta-2 adrenergic receptor gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:6120128
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adrenergic receptor
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Pred. No.
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RESULT 1
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VERSION
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Best Local S
Matches 19
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        Human mRNA for brain X04827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
Carnivora; Fissipedia; Canidae; Canis.
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Emala, C.W., Kuhl, J., Hirshman, C.A. and Levine, M.A.
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19; Conserv
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J. Anim. Sci. 74 (9), 2285 (1996)
  X04827.1
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LAIVFCNVLVITAIARFERLQTVTNYFITSLACADLVMGLAVVPFGASHILMKWWTFG
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I IMGTFTLCWLPFF I VNI VHV I QDNLI PKEVY I LLNWYGYVNSAFNPLI YCRSPDFRI
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John Hopkins Hospital,
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                                                                                                                                                                                                                                                                            Chung, F. 2., Lentes, K.U., Gocayne, J., Fitzgerald, M., Robinson, D., Kerlavage, A. R., Fraser, C.M. and Venter, J.C.
Cloning and sequence analysis of the human brain beta-adrenergic receptor. Evolutionary relationship to rodent and avian beta-receptors and porcine muscarinic receptors
FEBS Lett. 211 (2), 200-206 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kerlavage, A.R.
Direct Submission
Submitted (22-SEP-1987) to the EMBL/GenBank/DDBJ databases
                                                   Human gene for bete
Y00106
Y00106.1 GI:29370
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1 (bases 1 to 1970)
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Data kindly reviewed (22-SEP-1987) by Kerlavage A.R.
Location/Qualifiers
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gene for beta-adrenergic
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/note="pot.

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/note="pot.

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TVPSDNIDSQGRNCSTNDSLL"
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/note="pot. glucocorticoid-responsive element"
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/db_xref="GI:29373"
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1 (bases 1 to 2305)
Schoffield,P.R., Rhee,L.M. and Peralta,E.G.
Primary structure of the human beta-adrenergic receptor gene Nucleic Acids Res. 15 (8), 3636 (1987)
87203400
                                                                                           Sequence 1 from Patent A65720
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Schofield, P.R.
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YSRVFQEAKRQLQKIDKSEGRRHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="membrane spanning domain IV" 1385. .1450
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1712. .1774
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616 c 649 g 545 t
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CANINE beta 2- AND beta 3-ADRENERGIC RECEPTORS AND USE THEREOF Patent: WO 9735973-A 02-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human beta-2-adrenergic receptor mRNA,
m15169 J02728 m16106
m15169.1 GI:178201
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Lenzen,G., Pietri-Rouxel,F., Drumare, Marie-Francoise and
                                                                                                                                                                                                                                                                                                                                                               cDNA for the human beta 2-adrenergic receptor: a protein with multiple membrane-spanning domains and encoded by a gene whose chromosomal location is shared with that of the receptor for platelet-derived growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kobilka, B.K., Frielle, T., Dohlman, H.G., Bolanowski, M.A., Dixon, R.A., Keller, P., Caron, M.G. and Lefkowitz, R.J. Delineation of the intronless nature of the genes for the human and hamster beta 2-adrenergic receptor and their putative promoter
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3451)
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Homo sapiens (clone: pTF.) (tissue library: Evan Sadler) placenta
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87222338
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32.085 Million cell updates/sec
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Canine beta-2 adre
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   RESULT 2
Q13383/c
ID 913883
AC 013383;
DT 07 NOV-
DE 2C2719
EW W091122
PD 22-AUG-
PF 08-FEB-
PR 08-FEB-
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PR 12YMO-)
PI Sledzie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        PT Producing hybrid G protein coupled receptors - mammalian DNA
pT sequences encoding receptors having at least one domain replaced
pT by corresp. yeast domain used to transform yeast host cells
pS Disclosure; Page 27; 65pp; English.
CC concode a 5' end by an EcoRI adhesive end followed by the extracelular
CC verminal domain of the STE2 gene prod. contg. nucleotides 1-147 of the
CC yeast G protein-coupled protein gene joined to nucleotides 103-136 of
CC the human G protein-coupled protein gene joined to nucleotides 103-136 of
CC the human G protein-coupled protein gene joined to nucleotides 103-136 of
CC transparent were joined in a four-part ligation, to construct pHRS16.
CC fragment were joined in a four-part ligation, to construct pHRS16.
CC fragment were joined in a four-part ligation, to construct pHRS16.
CC adrenergic-STE2 hybrid receptor.
CC see also Q13381 and Q13383-83.
SQ Sequence 187 BP; 58 A; 36 C; 43 G; 50 T;
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Q13384;
O7-NOV-1991 (first entry)
ZC2720 oligonucleotide (pHRS17).
AR; adrenergic receptor; G-protein
W09112273-A.
22-AUG-1991.
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443
443
454
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                                                                                 07-NOV-1991 (first entry)
2C2719 oligonucleotide (pHRS17).
AR; adrenergic receptor; G-protein; ss.
W09112273-A.
22-AUG-1991.
08-FEB-1991; U00909.
08-FEB-1990; US-478100.
(ZYMO-) ZYMOGENETICS INC. Sledziewsk AZ, Sheppard PO; Sledziewsk AZ, Sheppard PO; WPI; 91-267100/36. Producing hybrid G-protein coupled receptors - mammalian DNA sequences encoding receptors having at least one domain replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sledziewsk AZ, Showpi, 91-267100/36
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08-FEB-1990; US-478100.
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Q80231
Q80226
T62781
Q80233
Q80228
Q80228
Q63879
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Q634524
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Pred. No.
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Rat NDF clone 41 D
Rat NDF clone 41 D
Rat NDF clone 19 D
Urea transporter p
Rat NDF clone 42B
Rat NDF clone 22 D
Polyhydroxyalkanoa
EST clone DN381. N
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                                                                                                 Pr Producing hybrid G-protein coupled receptors - mammalian DNA producing hybrid G-protein coupled receptors - mammalian DNA producing hybrid G-protein coupled receptors having at least one domain replaced pr sequences encoding receptors having at least one domain replaced pr by corresp. Yeast domain set of the ps Disclosure; page 37-38; 65pp; English.

The hybrid beta2AR-STE2 receptor was constructed by replacing the DNA compared to the extracellular N-terminal domain with a DNA compared encoding the extracellular N-terminal domain of the sequence encoding the extracellular N-terminal domain of the sequence encoding the extracellular N-terminal domain of the construct pHRS17 comprises this sequence together with a TPII construct pHRS17 comprises this sequence together with a TPII construct pHRS17 comprises this sequence together with a TPII construct pHRS17 comprises this sequence together with a TPII construct pHRS17 comprises this sequence together with a TPII construct pHRS17 comprises this sequence together with a TPII construct pHRS17 comprises this sequence together with a TPII construct pHRS17 comprises this sequence together with a TPII construct pHRS17 comprises this sequence together with a TPII construct pHRS17 construct pHRS18 construct pHRS17 construct pHRS18 construct pHRS18 construct pHRS18 construct pHRS18 construct pHRS18 construct pHRS18 cons
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Oligonucleorides 2C2719 and ZC2720 (Q13383-84) were designed to encode a 5' end by an EcoRI adhesive end followed by the extracellular encode a 5' end by an EcoRI adhesive end followed by the extracellular encode a 5' end by an EcoRI adhesive end followed by the extracellular encode a 5' end by an EcoRI adhesive end followed by the extracellular encode a 5' end by an EcoRI adhesive end followed by the extracellular encoding nucleotides 1-147 of the yeast G protein-coupled protein gene of conclectides 103-136 of the human G protein-coupled protein gene (see Q1381).
The oligonucleotides, the beta2AR fragment and the pMVR1 vector fragment were joined in a four-part ligation, to construct pHRS16. From pHRS16, construct pHRS17 is produced encoding the human beta2-adrenergic-STE2 hybrid receptor.
See also Q13881 and Q13383-83.
Sequence 191 BP; 52 A; 43 C; 36 G; 60 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-1991;
08-FEB-1991;
08-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human beta2-adrenergic-STR2 hybrid receptor (1).
AR; adrenergic receptor; G-protein; ligand; screening; internal; extracellular; N-terminal; C-terminal; effector; domain; ss.
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Q13381;
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      receptors are as follows: (1) the C-terminal intermal and C-terminal obmain is replaced; (2) the N-terminal extracellular and C-terminal internal effector domains are replaced; and (3) the N-terminal extracellular domain, the third internal effector domain and C-extracellular domain.
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148. .1287
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protein-coupled receptor"
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ID T93249;
DT T93249;
DT 20-APR-
DE Beta-2
KW Beta-2
KW asthmat
OS Homo sa
FH Key
FT CDS
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FT CTS
PN W097359
PN W097359
PN W07359
PN CCT-MAR
PR 27-MAR
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Sequence
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See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel beta-2 adrenalin receptor sub-type - useful for screening for agonists and antagonists and researching asthmatic diseases Claim 5; Page 23-26; 47pp; Japanese.
This sequence encodes the protein of the invention. The protein of the invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 125I-cyanopindrol. The protein can be used approximately 75 pM against 125I-cyanopindrol. The protein can be used screening for agonists and antagonists, which are useful in researching asthmatic diseases.

Sequence 1400 BP; 304 A; 402 C; 363 G; 328 T;
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24-MAR-1997;
27-MAR-1996;
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Beta-2 adrenalin receptor
Beta-2 adrenalin subtype;
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                 W09735963-A1.
02-OCT-1997.
24-MAR-1997; J00982.
27-MAR-1996; JP-072914.
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(DAIN
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                                                                                                                                                                                                                                                                                                                               PT Canino beta 2 and beta 3 adrenergic receptors and coding sequences - was full for identifying specific ligands and (ant)agonists to develop specific treatments for obesity in dogs

PT specific treatments for obesity in dogs

PT claim 1; Page 45-46; 79pp; French.

CC receptor (RA-Ca-b2) gene. The sequence was isolated from a cDNA library constructed from polyA+ RNA purified from dog brown adipose tissue cells.

CC The probe was a 600 bp fragment of the coding region of the human beta-3 cadrenergic receptor covering the region from the initiation codon to transmembrane domain 5 (TMS). The full length insert was cloned into M13 crossed e.g. in a mammalian cell, by subcloning into an expression vector such as pCDNA3. The beta-2 receptor can be used in comparative structure-function studies, e.g. for differential screening of ligands specific for RA-Ca-b2 or RA-Ca-b3 (W44933).

SO Sequence 2679 BP; 577 A; 736 C; 724 G; 642 T;
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Best Local 9
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02-0CT 1997.
26-MAR-1997; F00537.
26-MAR-1996; FR-003730.
(VETI-) VETICEN.
Drumare MF, Lenzen G, Pietri-Rouxel F, WPI; 98-032136/03.
P-PSDB; W44932.
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This sequence encodes the protein of the invention. The protein of the invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 125I-cyanopindrol. The protein can be used screening for agonists and antagonists, which are useful in researching asthmatic diseases.

Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T;
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hybridisation; ligand; 88.
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                                                                                                                                                                                                                                                                                                                                                                                             CC W75777) having an arginine residue at position 16. A novel method CC for identifying individuals susceptible to adverse responses to regular administration of beta-sponists comprises: (a) identifying CC in a genomic nucleic acid sample from the individual first and second alleles of the beta 2-adrenergic receptor gene, and (b) CC classifying an individual as susceptible if first and second CC classifying an individual as susceptible if first and second cC classifying an individual as susceptible if first and second cC identified by any known method e.g. denaturing gel electrophoresis CC or PCR amplification (see also v52615-17). Identification or preferably comprises amplifying a portion of each allele which CC includes the sequence encoding residue 16, and optionally also CC comprises determining nucleotide sequences of these portions (e.g. by automated sequence analysis). The invention identifies a known polymorphism in the beta 2-adrenergic receptor gene as being linked CC to adverse responses to regular beta-agonist administration; position 16 of the encoded protein can be either arg or Gly, and CC individuals homozygous for Argl6 are more susceptible.

Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T;
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                        v87532;
12-FEB-1999 (first entry)
EST clone DU675.
Expressed sequence tag; secreted protein; haematopolesis regulator;
tissue growth; activin; inhibin; tumour invasion suppressor; EST; h
chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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03-MAR-1997; US-811441.
(BGHM ) BRIGHAM & HOMENS HOSPITAL.
BOUShey H, Chinchilli VM, Drazen JM, Fish JE,
MARTIN RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beta2-adrenergic receptor protein
Disclosure; Page 33-35; 46pp; English.
This CDNA sequence codes for human beta-2-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing asthma patients predisposed to adverse beta reactions upon regular administration - by identifying homozygous for allele encoding Arg at position 16 of
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polymorphism; ds.
                              Homo sapiens.
W09845437-A2.
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11-SEP-1998.
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Human beta-2-adrenergic
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V52614;
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                                                                                                                                                                                                                                                          ACATGACGATGCCCATGCC
                                                                                                                                                                        standard;
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                                                                                                                                                                                                                                                                                                                       Conservative
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1633
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1588. .2829
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                                                                                                                                                                        CDNA; 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
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                                                                                                                                                                                                                                                                                                                                    Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                      DB 1
0.71;
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Best I
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             This sequence represents a partial human nucleotide sequence that codes for EZA binding protein (EZA-BP, see #35815). It was isolated from a human aortic expression library using the bHLH domain of E47 as probe. EZA-BP is expressed in vascular smooth muscle cells; mRNA is preferentially expressed in the aorta. EZA-BP interacts with EZA proteins in vivo, binds to both E12 and E47 and inhibits binding of E47 homodimer to an E-box probe (see T97606). A full-length DNA sequence is given in T97610, and mouse (see T97611) and rat (see T97612-13) EZA-BP sequences have also been isolated. EZA-BP nucleic acids may be used in gene therapy and antisense methods for treating vascular diseases such as arteriosclerosis, to produce transgenic or knock-out animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries
Claim 1; Page 95; 641pp; English.
The present sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy.
Sequence
                                                                                                                                                                                                                                                              DNA encoding human and mouse E2A binding proteins - useful for inhibiting or stimulating growth of vascular smooth muscle cells, e.g. for wound healing or treatment of rheumatoid arthritis or retinopathic diabetes
                                                                                                                                                                                                                                                                                                                                                                           15-MAR-1996; US-013439.
(HARD ) HARVARD COLLEGE.
Endege WO, Haber E, Layr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human E2A-binding protein genomic DNA (partial sequence). E2A-binding protein; E2A-BP; human; vascular smooth muscle cell; wound healing; angiogenesis; arteriosclerosis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haematopolesis regulating activity, tissue growth activity, activity, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition
                                                                                                                                                                                                                                                                                                                                          WPI; 97-470808/43.
P-PSDB; W36815.
                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-1997.
14-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity. The EST sequences are also stated to be useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agostino MJ, Jacobs K, Lavallie Racie LA, Spaulding V, Treacy M; WPI; 99-070078/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113
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nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
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                                                                                                                                                                                                                                           14; Page 47-51; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                           Haber E, Layne MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432 BP;
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 methods of
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94.7%;
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                               Lee M;
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E2A-BP polypeptides
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RESULT 10
T97610/c
TD T97610
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                                                                                                                                                    PT inhibiting or stimulating growth of vascular smooth muscle cells, PT e.g. for wound healing or treatment of rheumatoid arthritis or PT retinopathic diabetes
PS Claim 9; Page 55-60; 90pp; English.

CC This sequence represents a full-length nucleotide sequence that CC codes for human E2A binding protein (E2A-BP, see W36816). It CC was isolated from a human aortic RNA following 3 rounds of 5'RACE CC procedures. E2A-BP is expressed in vascular smooth muscle cells; CC with E2A proteins in vivo, binds to both E12 and E47 and inhibits CC with E2A proteins in vivo, binds to both E12 and E47 and inhibits CC with E2A proteins in vivo, binds to both E12 and E47 and inhibits CC binding of E47 homodimer to an E-box probe (see T97606). Mouse CC see T97611) and rat (see T97612-13) E2A-BP sequences have also been isolated. E2A-BP nucleic acids may be used in gene therapy CC and antisense methods for treating vascular diseases such as arteriosclerosis, to produce transgenic or knock-out animals, as CC well as in methods of producing E2A-BP polypeptides that can be used therapeutically to promote vascular smooth muscle cell growth CC e.g. for wound healing, or to screen for modulator compounds useful e.g. for the treatment of arteriosclerosis and angiogenesis. The CC E2A-BP gene promoter can be used in gene therapy methods to direct vascular smooth muscle cell-specific expression of the E2A-BP gene, antisense sequences or heterologous genes.

SQ Sequence 3854 BP; 899 A; 1214 C; 1161 G; 580 T;
                                                                    Query Match
Best Local S
Matches 16
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Best Local
2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding human and mouse E2A binding proteins - useful for inhibiting or stimulating growth of vascular smooth muscle cells, e.g. for wound healing or treatment of rheumatoid arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human E2A-binding protein cDNA.
E2A-binding protein; E2A-BP; human; vascular smooth muscle cell; wound healing; angiogenesis; arteriosclerosis; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be used therapeutically to promote vascular smooth muscle cell growth e.g. for wound healing, or to identify modulator compounds suitable for treatment of e.g. arteriosclerosis and angiogenesis. Sequence 2795 BP; 653 A; 828 C; 842 G; 472 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T97610;
27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; W36816
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Endege WO, Haber E, Layne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-1997.
14-MAR-1997; U04117.
15-MAR-1996; US-013439
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                                 4 tgacgatgcccatgcc
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TGACGATGCCCATGCC
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                                                                    16; Conservative
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100.0%;
2611
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                                                               ر. 0%;
0;
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                                                                    Score 16; DB; Pred. No. 23; 0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee
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                                                                                       DB 1;
23;
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22
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                                                                                                       Length 3854;
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RESULT Q43662 ID Q4

11

Q43662 standard; DNA; 4131 BP

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PT Tal R, Wong HC;
DR WPI; 93-197062/24.

DR P-PSDB; R38155, R38156.

PT Polynucleotide sequence from Acetobacter cdg operon - encodes proposed from the pro
        14-OCT-1992; U08756.
29-NOV-1991; US-800218.
(WEYE ) WEYERHAEUSER CO.
Ben-Bassat A, Benziman M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-1993 (first entry)
Acetobacter cdg3 operon.
Cyclic diguanylate; diguanylate phosphodiesterase;
diguanylate cyclase; cellulose production; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cde
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Key Loca
cds 387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q43662;
13-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- dgc3
/note- "a diguanylate cyclase gene;
/note- "a diguanylate cyclase gene;
the ORF is described as continuing to
nucleotide 4143 although the sequence is
only shown up to nucleotide 4231. The ami
acid sequence R38156 cannot be deduced
directly from this open reading frame whi
is given as printed in the specification"
ce 3848. .3850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon= seq:GGG;
3962. .3963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            743 will restore 2522. .2523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence"
741. .742
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the amino acid sequence R38155 cannot be
deduced directly from this open reading
frame due to a number of apparent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon= seq:CC; aa:Ala
/note= "insertion of G
2560 will restore the r
2657, .4131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon= seq:GG; aa: Trp
/note= "insertion of T betwee
/2522 will restore the reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon= seq: GT; aa: Val
/note= "insertion of N betwee
743 will restore the reading
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387. .2606
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Query Match

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PA (SANO) SANDOZ PATENT GMBH.

PA (COhen Y, Guegler K, Moesinger E, Niderman T;

PI (COhen Y, Guegler K, Moesinger E, Niderman T;

PI (COhen Y, Guegler K, Moesinger E, Niderman T;

PI (SANO) SANDOZ PATENT GMBH.

PI (SANO) SANDOZ PATENT T;

PI (SANO) SANDOZ PATENT T
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26-NOV-1992:
14-MAY-1992;
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                                                                                                 Pathogenesis-related protein P14a gupR-protein; fungicide; rust fungus;
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                                             signal_peptide
                                                                                  Lycopersicon esculentum.
                                                                                                                                       07-APR-1993 (first entry)
                                                                                                                                                                        Q31652 standard; cDNA; 480
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GB-010544.
                                             Location/Qualifiers
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Pred. No. 69;
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for treating fungal infection of e.g. Uromyces appendiculatus, PT Erysiphe graminis, etc. in plants
PS Claim 3; Page 22; 36pp; English.
CC A cDNA library was established from infected tomato plants. The CC library was screened for P14 genes using a probe (Q31657) based on CC the known P14 sequence (EMBO Journal, vol.4. #11, 2745-2749, 1985).
CC A positive clone containing an ORF of 480bp was isolated and CC sequenced. It was found to encode P14a, a 159 amino acid protein CC differing from the previously published P14 protein by 5 additional CC amino acids (at AA positions 99-103, inclusive). The P14a CDNA was CC used to screen a genomic library for other members of the P14 CC family P14a has fungicidal activity and can be used to combat rust CC see Q31652-031660.
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Matches 16
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26-MOV-1992: E01063.
14-MAY-1992: E01063.
15-MAY-1991; GB-010544.
(SANO) SANDOZ LTD.
(SANO) SANDOZ PATENT GMBH.
(SANO) SANDOZ PATENT GMBH.
COhen Y, Guegler K, Moesinger E
WPI; 92-415778/50.
P-PSDB; R28350.
                                                                                                                                         06-JAN-1994.
29-JUN-1993; U06228.
29-JUN-1993; US-907138.
30-UN-1992; US-940389.
23-OCT-1992; US-955173.
24-MAR-1993; US-95555.
(CAMB-) CAMBRIDGE NEUROSCIENCE.
(CAMB-) LUDWIG INST CANCER RES.
ChupM-) LUDWIG INST CANCER RES.
Chen MS, Goodearl A, Hiles I, Stroobant P, Waterfield M;
WPI; 94-025882/03.
                                                                             Glial mitogenic polypeptide factors glial cell mitogenesis and treating claim 1-21; Fig 31; 178pp; English. The DNA sequence encoding a polypept
                                                                                                                                                                                                                                                                                                                                                      GGF gene coding segment L.
Glial growth factor; GGF; heregulin; mitogenesis;
Schwann cell; tumour; central nervous system; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                     Q66939
wherein WYBAZCX is composed of the polypeptide sequences R55639-53 and R55766-75, wherein W comprises polypeptide segment F, or wherein Y comprises polypeptide segment E, or wherein Z comprises polypeptide segment G, or
                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                          Q66939
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                                                                   WYBAZCX
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Pred. No. 70;
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17-FEB-1994.
10-AUG-1993; US-927337.
10-AUG-1992; US-927337.
25-SEP-1992; US-951747.
01-DEC-1992; US-91747.
29-JAN-1993; US-011396.
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Sequence
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WPI; 94-065731/08.
P-PSDB; R55815.
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GGF gene cod
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Claim 6-7, 21-24; Fig 31; 178pp;
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                                                                                                                                                                                                            Polypeptides
VYBAZWX
                                                                                                                                                                                                                                                                                                                                                         (CAMB-) CAMBRIDGE NEUROSCIENCE INC.
     polypeptides comprising FBA, FBA', segments are used for inhibiting p
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16; Conservative
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factor; GGF; heregulin; proliferation; antibody;
; tumour; central nervous system; inhibition;
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          EBA', FEBA or FEBA' polypeptide
eration of a cell, for producing
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/' HKL, C/D D', HKL,
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for treating
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                         Issued_Patents_NA:*

1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

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23.141 Million cell updates/sec
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/cgn2_6/ptodata/1/lna/5B_COMB.seq:*
/cgn2_6/ptodata/1/lna/5C_COMB.seq:*
/cgn2_6/ptodata/1/lna/5C_COMB.seq:*
/cgn2_6/ptodata/1/lna/5C_COMB.seq:*
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PCT-US92-08756A-3
US-08-036-555B-77
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US-08-469-526A-77
US-08-469-526A-77
US-08-734-591A-77
US-08-469-660-182
PCT-US94-05083C-178
PCT-US94-05083C-178
PCT-US95-06846A-77
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              US-08-440-401-10
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US-08-096-277-6
US-08-550-815-6
US-08-73-089-6
US-08-73-089-7
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PCT-US91-00909-3
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Best Local Similarity 100.
Matches 19; Conservative
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74.7	74.7	74.7	74.7	74.7	74.7	74.7		75.8				75.8						77.9
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ALIGNMENTS

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RESULT 1
PCT-US91-00909-21
; TOPOLOGY: 11; MOLECULE TYPE: PCT-US91-00909-21
                                                  TELEFAX: 206-682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 187 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application PC/TUS9100909 GENERAL INFORMATION:
                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US91/
FILING DATE: 199.10208
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 9900
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CONTROL OF TOWN OF THE POST/US91/00909
                                                                                                                                                                                                  TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sledziewski, Andrzej Z.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Methods of Producing Hybrid
TITLE OF INVENTION: Protein-Coupled Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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PCT-US91-00909-20/c
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GENERAL INFORMATION:
APPLICANT: Sledziewski, Andrzej Z
APPLICANT: Sheppard, Paul O.
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Best Local
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LENGTH: 191 base pairs
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                      COMPUTER READABLE FORM:
                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                         APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Methods of Producing Hybrid G
TITLE OF INVENTION: Protein-Coupled Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 99
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Sheppard, Paul
                                                                                                                                                                                                                                                                                                                                                           176 ACATGACGATGCCCATGCC 158
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                                                                                                                                                                NUMBER OF SEQUENCES:
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                                      COUNTRY: United ZIP: 98104-7092
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CLASSIFICATION: 435
                                                                                                          STREET:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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6300 Columbia Center, 701 Fifth Ave
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                                                         United States
                                                                                                                                                                                                                                    Sledziewski, Andrzej Z.
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Protein-Coupled Receptors
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Pred. No. 0.76;
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                                               CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/
APPLICATION NUMBER: 1991
TANGE DATE: 29-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Tal, R
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 9900
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                         ATTORNEY/AGENT INFORMATION:
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TITLE OF IN
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                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                       MEDIUM TYPE:
REFERENCE/DOCKET NUMBER:
             NAME: Bortner, Scott R. REGISTRATION NUMBER: 34,298
                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                  COUNTRY:
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les 19; Conserv
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TOPOLOGY: lir
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SOFTWARE: Patentl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                   94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                        INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08309512
                                                                                                                                                                                                                                                                                             E: Pennie & Edmonds
2730 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1242 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206-682-6031
                                                                                                                                                                                                                                                                                                                                                                    wong,
                                                                                                                                                                                                                                                                                                                                                                                 Calhoon, Roger D.
                                                                                                                                                                                                                                                                                                                                                                                                              Gelfand, David H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                 Ben-Bassat,
                                                                                                                                                                                                                                                                                                                                                                                                                          Benziman, Moshe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                      Floppy disk
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                                                                                                                                                                                                                                                                                                                                                       CYCLIC DIGUANYLATE METABOLIC ENZYMES
                                                                                                                                                                                                                                                                                                                                          63
                                                                       us 07/800,218
                                                                                                                                us/08/309,512
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8145-008
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Pred. No. 0.89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
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                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION NUMBER: PCT/US92/08756A
FILING DATE: 19921014
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/800,218
FILING DATE: 29-NOV-1991
ATTORNET/AGENT INFORMATION:
NAME: NOTTO: SCOTT B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                    TELEX: 278356
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4131 base pairs
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                     NAME: BOTTNEY, SCOTT R. 34,298
REGISTRATION NUMBER: 34,298
REFERENCE/DOCKET NUMBER: WE'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: CYCLIC DIGUANYLATE
TITLE OF INVENTION: CYCLIC DIGUANYLATE
TITLE OF INVENTION: METABOLIC ENZYMES
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 4131 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Benziman, Moshe
Gelfand, David H.
Ben-Bassat, Arie
Calhoon, Roger D.
                                                                   415-433-8716
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94.1%; Pred. No. 4
                                                                                                                                                                                                                                                                                 PCT/US92/08756A
                                                                                                                          WEYR 20050 USA
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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Acetobacter xylinum
PCT-US92-08756A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                         TELEFAX: (212) 838-3884 NFORMATION FOR SEQ ID NO:
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                                                                                                                               APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
NAME: T9a1, Christine H.
REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: LUD 5250.4
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION NUMBER: 07/940,389
PRITTY NOTE: 07-25: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM.TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
                      SEQUENCE CHARACTERISTICS:
LENGTH: 730
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
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ANTI-SENSE: |
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/940,389 FILING DATE: 03-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette,
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                                                                                             688-9200
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94.1%;
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Pred. No. 4
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US-08-036-555B-77

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; TOPOLOGY: US-08-469-569-77
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WOrdperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 06-JUN-1995
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APPLICANT: Chen, Maic
TITLE OF INVENTION: (
TITLE OF INVENTION: (
                                                                                                           TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/940,389 FILING DATE: 03-SEP-1992 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 07/863,703
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                                       STRANDEDNESS:
                                                                                                                                                                                                                                                     APPLICATION NUMBER: U.K. 91 07566.3 FILING DATE: 10-APRIL-1991
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 30-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York City
STATE: New York
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                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Conservative
                                                      nucleic acid
                                                                                                                                                                                                                     Tsai, Christine H.
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805 Third Avenue
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Chen, Maio Su; Hiles, Ian
NYENTION: Glial Mitogenic Factors, Their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
                    linear
                                                                                                                                               (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                              03-APRIL-1992
                                                                                                                                                                                                                                                                                                                                                                     UMBER: 07/907,138
30-JUN-1992
                                   single
                                                                                                                                               688-9200
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                                                                                                                                                                                   LUD 5250.4
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Pred. No. 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Query Match

77.9%;

Score 14.8;

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Length 730;

Mismatches

Indels

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Gaps

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US-08-249-322A-77
                                                                                                   US-08-249-322A-77
Query Match
Best Local Similarity 80...
Thes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                              TELEFAX: (212) 838-3884
INFORMATION FOR SFQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM
OPERATING SYSTEM: PC-DC
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: U.K. APPLICATION NUMBER: 10-APRIL-199
ATTORNEY/AGENT INFORMATION:
NAME: Tsai, Christine H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                           REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23-OCT-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/0:
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 805 Third Avenue CITY: New York City
                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                 LENGTH:
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                                                                                                                                              nucleic acid
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Chen, Maio Su; Hi
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minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
                                                                                                                     linear
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                                                                                                                                                                                                                                 (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1992
                                                                                                                                                                                                                                                                                                                           UMBER: U.K. 91 07566.3
10-APRIL-1991
                                                                                                                                                                                                                                                                                                                                                                             UMBER: 07/863,703
03-APRIL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1992
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                                                                                                                                 single
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                                    77.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/249,322A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07/965,173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.25 inch, 360 kb storage
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                                       Score 14.8;
Pred. No. 80;
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                                                      DB 2;
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                                                        Length 730;
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106 CATGACGGTGTCCATGCC 123

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; OTHER INFORMATION:
US-08-469-526A-77
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                                                                                                   Matches
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: U.K. 91 07:
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bleker-Brady, Kristina
RECISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-428-7045
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
APPLICATION NUMBER: 07/907,138
FILING DATE: 03-JUN-1992
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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106 CATGACGGTGTCCATGCC 123
                                                                                                                        Local Similarity 88.9%;
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ZIP: 02110
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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2 catgacgatgcccatgcc 19
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176 Federal Street
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Waterfield, Michael
Marchionni, Mark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goodearl, Andrew
                                                                                                   Conservative
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                                                                                                                                   Score 14.8;
Pred. No. 80
                                                                                                   Mismatches
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                                                                                                                                                               Length 730;
                                                                                                   Indels
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                                                                                                   Gaps
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RESULT 10
US-08-734-591A-77
; FEATURE:
; OTHER INFORMATION:
US-08-734-591A-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION NUMBER: 07/940,389
APPLICATION NUMBER: 07/940,389
APPLICATION NUMBER: 07/940,389
APPLICATION NUMBER: 07/940,389
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                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/03
APPLICATION NUMBER: 08/03
                                                                                                                                                                               NAME: Bleker-Brady, Kristina REGISTRATION NUMBER: 39,109 REFERENCE/DOCKET NUMBER: 04585/00200P TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 428-0200 TELEFAX: (617) 428-7045
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: UK 91 07566.3

FILING DATE: 10-APR-1991

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect (Version 7.0) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/734,591A
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible Pentium
OPERATING SYSTEM: Windows95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 730
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR TITLE OF INVENTION: PREPARATION AND USE NUMBER OF SEQUENCES: 187
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/863,703 FILING DATE: 03-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                  TOPOLOGY:
                                                                         STRANDEDNESS:
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                                                                                        nucleic acid
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Minghetti, Luisa
Waterfield, Michael
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                                                    linear
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22-OCT-1996
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06-JUN-1995
                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                              07/907,138
                                                                                                                                              77:
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Query Match

Local

Similarity

77.9%;

Score 14.8; Pred. No. 80;

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Length 730;

Mismatches

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Conservative

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US-08-469-660-182
В
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                                                                      Matches
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APPLICATION NUMBER: 08/011,396

FILING DATE: 29-JAN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/984,085

FILING DATE: 01-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/951,747

APPLICATION NUMBER: 07/951,747
                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION UNMER: 07/927
FILING DATE: 10-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    TELEFAX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gwynne, David I.; Marchionni, Mark; APPLICANT: McBurney, Robert N.
TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION, TITLE OF INVENTION: THEIR PREPARATION AND USE NUMBER OF SEQUENCES: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04585/017004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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ZIP: 0211-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 catgacgatgcccatgcc 19
106 CATGACGGTGTCCATGCC 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/469,660
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                                                                                         Local
                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                  LENGTH:
                            2 catgacgatgcccatgcc 19
                                                                      16;
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                                                                                         Similarity
                                                                                                                                                                                                                 nucleic acid
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225 Franklin Street
                                                                        Conservative
                                                                                                                                                                                linear
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                                                                                                                                                                                              double
                                                                                         77.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                    07/927,337
                                                                        0;
                                                                                         Score 14.8;
Pred. No. 80;
                                                                          Mismatches
                                                                                       No.
                                                                                                            DB 3;
                                                                                                            Length 730;
                                                                            Indels
                                                                            Gaps
                                                                               0;
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RESULT 12

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PCT-US94-05083C-178
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GENERAL INFORMATION:
APPLICANT: Robert Sklar, Mark Marchionni,
AppLICANT: David I. Gwynne
TITLE OF INVENTION: METHODS FOR ALTERING
TITLE OF INVENTION: MUSCLE CONDITION
                                                                                                                                                                                                                                                                                          PCT-US95-06846A-77
                                                                                                                                                                                                                                                 Sequence 77, Application PC/TUS9506846A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-May-93
ATTORNEY, AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 04585/028W01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,204
FILING DATE: 08-MAR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059,022
FILING DATE: 06-May-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
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                                                                                                                               APPLICANT: Goodearl, Andrew David; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                      106 CATGACGGTGTCCATGCC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
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ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                              ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nuclear
                                                                                                                                                                                                                                                                                                                                                                                           2 catgacgatgcccatgcc 19
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COUNTRY: UZIP: 10022
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                    USA
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Pred. No. 80;
0; Mismatches
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

Diskette,

5.25 inch,

360 kb storage

OPERATING SYSTEM: PC-DOS

Wordperfect

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Best Local S
                                                                                                                                                                                                                                          Sequence 6, Application US/07640476 Patent No. 5376536
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: QUAX, WILHELMUS
APPLICANT: LUITEN, RUDOLF G.M.
APPLICANT: SCHUURHUIZEN, PAUL W.
APPLICANT: MRABET, NADIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/036,555
FILING DATE: 24 MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
ADDITION NUMBER: PCT/US95/06846A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: HANBON, NORMAN D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
                                                               ADDRESSEE: Morrison
                                                                                                  TITLE OF INVENTION: NOVEL GLUCOSE TITLE OF INVENTION: THEIR USE NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 10-APRIL-19:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.K. 91 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 25-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,322
FILING DATE: 26-MAY-1994
                                                                                                                                                                                                                                                                                                                                                   106 CATGACGGTGTCCATGCC 123
                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                         16;
              Menlo Park
CA
                                                                                                                                                                                                                                                                                                                                                                                                                                       n 77.9%;
Similarity 88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                  545
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                               Morrison & Foerster
5 Middlefield Road, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: U.K. 91 07566.3
10-APRIL-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14.8;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                      ISOMERASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         6,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 730;
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                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/07847743B Patent No. 5367060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Genentech,
TITLE OF INVENTION: S:
TITLE OF INVENTION: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA MOLECULE TYPE: DNA
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Street
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                       NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD:
OTHER INFORMATION: /EC_
OTHER INFORMATION: /prc
OTHER INFORMATION: /eva
OTHER INFORMATION: /sta
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                                                                                                                                                                                                                                                                                                                                                                                                                             249 CATGACGGTGCCCATGGC 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kate H. Murashige REGISTRATION NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 19910:
                                                                                                         COUNTRY: U
                                                                                                                                          STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                               2 catgacgatgcccatgcc 19
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88.9%;
                                                                                                                                                                                                                                                                  Structure,
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CC_number= 5.3.1.5

/product= "xylose isomerase (glucose isomerase)"

/evidence= EXPERIMENTAL
/standard_name= "D-xylose ketol isomerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/07/640,476
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Pred. No. 83;
0; Mismatches
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                                                                                                                                                                                                                                                                  Production and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1164;
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APPLICATION NUMBER: US/07/847,743B

FILING DATE: 19920366

CLASSIFICATION: 424

PRICE APPLICATION NUMBER: 07/765256

APPLICATION NUMBER: 07/765256

PRICE APPLICATION NUMBER: 07/765256

PRICE APPLICATION NUMBER: 07/765212

PRICE APPLICATION NUMBER: 07/765212

PRICE APPLICATION NUMBER: 07/765212

PRICE APPLICATION NUMBER: 07/765212

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 1000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
υS-09-542-718-3
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 September 12, 2000, 22:46:44; Search time 1893.64 Seconds (without alignments) 44.246 Million cell updates/sec
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and is derived by analysis of the total score distribution.
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AW424650 707020G08
C82152 C82152 Leuk
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AU064022 AU064622
AI958009 Fc89ell y
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AW421540 fj92f07 y
AW421555 Fugu rubr
AI444197 fb44hll y
AQ560764 HS_2079_B
AQ167783 HS_203_B
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AQ167783 HS_203_B
AQ162781 mh49hll r
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AQ666234 HS_5359_B
AA603161 np55e04.s
AL026701 Fugu rubr
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AI444193 fb44904 y
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AJ272869 AJ272869
AV391075 AV391075
AQ937984 NB6-748R
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AW134110 fi16d03.y
AW343389 fi76h11.y
AA246435 LD05332.5
AW343362 fi76f07.y
AL065380 Drosophil
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ACCESSION
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Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
Maekawa,H., Nakamura,Y. and Takahashi,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A1870022 522 bp mRNA EST 07-MAR-2000 w163h10.x1 KCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429631 similar to SW:NPLZ_MOUSE P51860 NUCLEOSOME ASSEMBLY PROTEIN 1:-2; contains element MER22 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Otsuka cDNA project
Unpublished (1996)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Tsutomu Fujiwara
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 820 Std Error: 0.00
                                                                                                                                                                                                                                              Unpublished (1998)
On Jan 19, 1998 this sequence version Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae
1 (bases 1 to 522)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                               National Cancer Institute / National Institute of Neurol
Disorders and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                                                                                                      Tissue Procurement: David N. Louis,
                                                                                                                                                       cDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                              Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="placenta"
113 c 101 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="GEN-559E06"
/clone_lib="Human placenta.cDNA (Trujiwara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 15;
Mismatches
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 1064 row: N column: 5
Seq primer: T?
Class.
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                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                            On Mar 23, 1999 this sequence version Contact: Mahairas GG, Wallace JC, Hood
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GSS.
               High quality sequence stop: 556.
Location/Qualifiers
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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/db_xref="taxon:9606"
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94.7%;
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Adams,M.D.
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Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
On Oct 6, 1998 thi
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
1 (bases 1 to 612)
                                                                                                                                                                                                                                                                                                                                                                                                                         Email: walbot@stanford.edu
Plate: 707020 row: G col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize ESTs from various cDNA libraries sequenced at Stanford University
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                                                                                             /note-*Organ: tassel, kernel, silk, husk, root, leaf; vector: pGADJ0; Site_1: ECORI; cDNA library from fully differentiated malze tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned.*

a 171 c 185 g 108 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=1064 Col=5 Row=N"
/clone_lib-"RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                /db_xref="taxon:4577"
/clone_lib="707 - Mixe
                                                                                                                                                                                                                        /lab_host-"DH10B"
                                                                                                                                                                                                                                      /tissue_type="tassel, kernel, silk, husk,
/dev_stage="adult"
                                                                                                                                                                                                                                                                                    (SK)
                                                                                                                                                                                                                                                                                                                                              /cultivar="W23"
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                                                                                                                                                                                                                                                                                                                                                               ∕organism-"Zea mays"
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  86.38;
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94.48;
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Score 16.4; DB Pred. No. 3e+02;
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Pred. No. 2.
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                  72;
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                      612;
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Mismatches

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Gaps

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C82152
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C82248
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Nam, B., Katagiri, T., Hong, Y., Hirono, I. and Aoki, T. A survey of expressed genes in the leukovyte of Japanese flounder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C82152 800 bp mRNA C82152 Leukocyte of Japanese clone WH11-3, mRNA sequence.
                                                                           Paralichthys olivaceus.

Paralichthys olivaceus.

Paralichthys olivaceus.

Paralichthys olivaceus.

Paralichthys olivaceus.

Euteleostei; Euteleostei; Neoteleostei;

Rotinopterygii; Neopterygii; Teleostei; Euacanthomorpha;

Eurypterygii; Ctenosquamata; Acanthomorpha;

Holacanthopterygii; Acanthopterygii; Percomorpha;

Holacanthopterygii; Acanthopterygii; Percomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
17; Conserv
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On May 11, 1999 this sequence version replaced gi:4776626.
Contact: Takash Aoki
Genetics and Biochemistry
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Paralichthys olivaceus
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                                                                                                                                                                                                                           clone WD3-5, mRNA sequence.
C82248
C82248.1 GI:5039484
                                                                                                                                                                                                                                                                                 C82248 Leukocyte of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ad95217@s4201.tokyo-u-fish.ac.jp
clone WH11-3: similar to human KIAA0174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tokyo University of Fisheries
Konan, 4-5-7, Minato 108, Japan
                                                      pleuronectiformes; Pleuronectoidei; Bothidae; Paralichthys.
1 (bases 1 to 940)
                                                                                                                                                                                                       EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Paralychthys olivaceus) infected with Hirame rhabdo virus
(Paralychthys olivaceus) infected with
                                  Nam, B., Katagiri, T.,
                 survey of expressed genes in the leukocyte of Japanese flounder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Paralichthys olivaceus"
/db_xref="taxon:8255"
/clone="WH11-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Leukocyte of Japanese flounder i"
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94.4%;
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                                    Hong, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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Pred. No. 3.1e+02;
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                                      Hirono, I. and Aoki, T.
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   Hirame rhabdo
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Contact: Takashi A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics and Biochemistry
Tokyo University of Fisheries
Konan, 4-5-7, Minato 108, Japan
Tel: 03-5463-0556
                                                                                                                                                                                                 Email: est@watson.wustl.edu
Insert Size: 1655
High quality sequence stops: 153 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1655
Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1995)
On Dec 20, 1995 this sequence version replaced gi:1133491.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 214)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R35420 214 bp mRNA E y965e10.r1 Soares infant brain lNIB Homo IMAGE: 38075 5', mRNA sequence.
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17; Conserv
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clone WD3-5: similar to human KIAA0174
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314 286 1810
                                                                                                                                              quality sequence stop: 153.
Location/Qualifiers
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/db_xref="taxon:8255"
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                                  /clone_lib="Soares infant brain
                                                       /db_xref="taxon:9606"
/clone="IMAGE:38075"
                                                                                        /organism="Homo sapiens"
/db_xref="GDB:410616"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="leukocyte
258 c 211 g
                   /sex="female"
/dev_stage="73 days post natal"
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94.48;
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The FAPESP/LICR Human Cancer Genome Pro
Unpublished (1999)
On Jul 7, 1999 this sequence version ro
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                            Email: asimpson@lidwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RClst2=RCl-BT0077-
150999-001-H05&t3-1999-09-15&t4=1)
Seq primer: puc 18 forward
High Cashier puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922
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                 36
             /note-*Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.*

a 80 c 93 g 57 t
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/db_xref-"taxon:9606"
/clone_lib-"BT0077"
                                                                                                                                                               /dev_stage="Adult"
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4.1e+02;
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Query Match

Best Local Similarity

84.2%; 100.0%;

Score 16; Pred. No.

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Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis
                                                                            (bases 1 to 463)

Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiems

EST (Koehrer, et al.)

Unpublished (199)

On Jan 19, 1998 this sequence version replaced gi:2285034.
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1 (bases 1 to 281)
Nishiguchi,S., Joh,T., Horie,K., Zou,Z., Yasunaga,T. and Shimada,K. A survey of genes expressed in undifferentiated mouse embryonal carcinoma F9 cells; characterization of low-abundance mRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Apr 7, 1998 this sequence version replaced gi:3036588.
Contact: Kazunori Shimada
Department of Medical Genetics, Division of Molecular Blomedicine
Research Institute of Microbial Diseases, Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                  Contact: Koehrer
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Mammalia; Eutheria; Primates;
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/db_xref="taxon:10090"
/clone="73A02"
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                                                                                                                                  Gassenhuber, J. and Wiemann, S.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?t1-PM3&t2-PM3-LT0031-
100100-003-d04&t3=2000-01-10&t4=1)
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Pr
Unpublished (1999)
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PM3-LT0031-100100-003-d04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Jan 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                 /note="Organ: leiomios; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="DKF2p586G622"
/clone_lib="586 (synonym:
/tissue_type="uterus"
/dev_stage="adult"
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
                                                                                                                        /dev_stage="Adult"
                                                                                                                                                /clone_lib="LT0031"
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cDNA amplification
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                                                        4 tgacgatgcccatgcc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Second distribution: NCI-CGAP clone distribution in found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1453 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 440.
Location/Qualifiers
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16; Conservative
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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1 (bases 1 to 582)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                        Conservative
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/Clone_lib="NCI_CGAP_Pr23"
/clone_lib="NCI_CGAP_Pr23"
/sex="male, pooled"
/tissue_type="prostate tumor"
/lib_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
/lab_hos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robert_Strausberg@nih.gov
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/db_xref="taxon:9606"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library availability, please contact Pleter de Jong (pletcr@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h GenetLes (lnfo@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 935 row: J column: 1 Seg primer: 77 Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
7cl: (206) 616-3618
7ax: (206) 616-3887
Email: jwailace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ666234 G49 bp DNA GSS 23-JUN-1999
HS_5359_B1_E01_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=935 Col-1 Row=J, genomic survey sequence.
                                                                          AA603161 335 bp mRNA np55e04.81 NCI_CGAP_Br1.1 Homo sapiens c similar to gb:D21261 SM22-ALPHA HOMOLOG AA603161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Dec 15, 1999 this sequence version replaced gi:4575425. Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 649) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahairas,G.G., Wallace,J.C., Young,J., Zhao,S., Adams,M.D. a. (Caler,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a.
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16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
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IMAGE:1130238
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On Jan 19, 1998 this sequence version replaced g1:2045715
Contact: Robert Strausberg, Ph.D.
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17; Conserv
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cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Cente: Clone distribution: NCI-CGAP clone distribution information can I found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                      Fugu rubripes
Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygil;
Neopterygil; Teleostel; Euteleostel; Acanthopterygil; Per
Tetraodontiformes; Tetraodontoidel; Tetraodontidae; Fugu.
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Fugu rubripes
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Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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1 (bases 1 to 335)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                         Williams, G. and Brenner, S. Direct Submission
                                                             1 (bases 1 to 341)
Elgar, G., Clark, M., Smith, S.,
                                                                                                                                                                                             GSS; genome sur
Fugu rubripes.
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Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone-"IMAGE:1130238"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host-"DH10B"
(09-JUN-1998) MRC Human Genome Mapping Project Resource
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Centre, Hinxton, Cambridge, CB10 1SB, UK. Email:
blobalp@hamp.mrc.ac.uk
vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
Location/Qualifiers
1. 341
1. 341
1. 341
2. Location_Punism="Fugu rubripes"
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//Clone="079M18bC12"
PBASE COUNT
70 a 105 c 87 g 79 t
ORIGIN

Ouery Match
B83.2%; Score 15.8; DB 122; Length 341;
Best Local Similarity 89.5%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps
0;
1 acatgacgatgcccatgcc 19
Db 262 ACATGATGATGCCCATGAC 280

Search completed: September 12, 2000, 22:46:49
Job time: 3791 sec
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September 12, 2000, 23:02:50; Search time 930.45 Seconds (without alignments) 28.772 Million cell updates/sec
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em_un: *
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em_htg1: *
gb_htg1: *
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gb_h1: *
em_hum4: *
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75: 76: 77: 79: 80: 81:	60: 61: 632: 643: 654: 667: 700: 711:	
gb_htg26:* gb_htg27:* gb_htg28:* gb_htg29:* gb_htg30:* gb_htg31:* gb_htg1:*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                                                                                                                                                             Green, S.A., Cole, G., Jacinto, M., Innis, M. and Liggett, S.B. A polymorphism of the human beta 2-adrenergic receptor within the fourth transmembrane domain alters ligand binding and functional properties of the receptor J. Biol. Chem. 268 (31), 23116-23121 (1993)
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens beta2-adrenergic receptor (ADRB2) gene, AF022954
AF022954.1 GI:2570528
                                                                                                                                                                                3 (bases 1 to 1242)
Green, S.A., Turki, J., Innis, M. and Liggett, S.B.
Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory propert
                                                                                                                                                                                                                                                                                           Am. J. Respir. Cell Mol. Biol. 8 (3), 334-339 (1993)
                                                                                                                                                                                                                                                                                                      Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S.B. Mutations in the gene encoding for the beta 2-adrenergic in normal and asthmatic subjects
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1242)
                                                                                                                        Erratum:[[published erratum appears in Biochemistry 1994 Nov 29;33(47):14368]]
4 (bases 1 to 1242)
Liggett, S.B. and Green, S.A.
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                                                                                               Submitted (04-SEP-1997) Medicine, Ave ML670564, Cincinnati, OH 4526
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Green,S.A., Turki,J., Innis,M. and Liggett,S.B.
Amino-terminal polymorphisms of the human beta 2-adrenergic receptor impart distinct agonist-promoted regulatory propert Biochemistry 33 (32), 9414-9419 (1994)
94347707
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1 (bases 1 to 1242)

Reihsaus, E., Innis, M., MacIntyre, N. and Liggett, S. B.

Rutations in the gene encoding for the beta 2-adrenergic receptor in normal and asthmatic subjects
in J. Respir. Cell Mol. Biol. 8 (3), 334-339 (1993)
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IIMGTFTLCWLDFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
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1 (bases 1 to 1242)

1 (bases 1, Innis, M., MacIntyre, N. and Liggett, S.B. Mutations in the gene encoding for the beta 2-adrenergic receptor in normal and asthmatic subjects
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Liggett, S.B. and Green, S.A.
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1 (bases 1 to 2305)
Schofield, P.R., Rhee, L.M. and Peralta, E.G.
Primary structure of the human beta-adrenergic receptor gene Nucleic Acids Res. 15 (8), 3636 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission Submitted (20-OCT-1987) to the EMBL/GenBank/DDBJ databases
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15; Conserv
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LAIVFGNVLVITAIAKEERLGTTYNYEITSLACADLVMGLAVVPFGAAHILMKMMTFG
NEWCEEWTSIDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVILLAWWY
SGLISELPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
/note="N-linked glycosylation site" 836...844
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IIMGTFTLCWLPFFIVNIVHYIQDNLIRKEYYILLMWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHYEQEKENKLLCEDLPGTEDFYGHQG
                                                                                                                                                                         /translation="MGOPGNGSAFILAPNRSHAPDHDVTOORDEVWVVGMGIVMSLIV
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VRFMCEFWTSIDVLCVTASIEFILCVIAVDRYFAITSPFKYGSLLTKNKARPILILMVWFV
SGLTSFLPIOMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
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/note="Thr164 to Ile polymorphism"
/replace="c"
330 c 325 g 311 t
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/protein_id="AAB82151.1"
/db_xref="GI:2570533"
                                                                                                 YSRYFQEAKRQLQKIDKSEGRFHYQNLSQYEQDGRTGHGLRRSSKFCLKEHKALKTLG
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AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFYGHQG
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/db_xref="SWISS-PROT:P07550"
                                                                                                                                                                                                                                                                                                                                                           /note="beta-adrenergic receptor (AA 1 - 413)"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                 794. .2035
                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Maniatis human"
/clone="lambdahbetaAR17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3451)

Kobilka, B.K., Frielle, T., Dohlman, H.G., Bolanowski, M.A., Dixon, R.A., Keller, P., Caron, M.G. and Lefkowitz, R.J.

Delineation of the intronless nature of the genes for the human and hamster beta 2-adrenergic receptor and their putative promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adrenergic receptor. Homo sapiens (clone: pTF.) (tissue library: Evan Sadler) placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human beta-2-adrenergic M15169 J02728 M16106
                                                                                                                                                                                                                                                                   cDNA for the human beta 2-adrenergic receptor: a protein with multiple membrane-spanning domains and encoded by a gene whose chromosomal location is shared with that of the receptor for platelet-derived growth factor platelet-derived growth factor Proc. Natl. Acad. Sci. U.S.A. 84 (1), 46-50 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 262 (15),
87222338
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Bolanowski,M.A., Sigal,I.S., Yang-Feng,T.L., Francke,U.,
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1712. .1774
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/note="membrane spanning
1007. .1078
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616 c 649 g 545 t
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1247. .1315
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                             1369.
                                                                                                                                          /tissue_type="placenta"
/tissue_lib="Evan Sadler"
                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="b-2-adr mRNA (alt.);
                                                              1369
                                                                           /gene="ADRB2"
/note="b-2-adr mRNA (alt.);
                                                                                                                       map="5q31-q32"
                                                                                                                                                                      'clone="pTF."
             'gene="ADRB2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis, Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
of segments is not known; 800 n's separate segments.

* NOTE: This is a 'working draft' sequence

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                 jes@sanger.ac.uk or rw@nematode.wustl.edu
On Oct 7, 1997 this sequence version replaced g1:2464982.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progr
                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (03-OCT-1997) Nematode Sequencing Project, Sanger Submitted (03-OCT-1997) Nematode Sequencing Project, Sanger Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z99713.1 GI:2467102
HTG; HTGS_PHASE1.
                                                                                                                         with foreign sequence from E.coli, yeast, vector, phage etc. Order
                                                                                                                                                                    contaminated
                                                                                                                                                                                                    the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sulston, J.
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                                                                                                                                                                                                 sequence may change as work continues.
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//db_xref="GDB:G00-120-541"
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/translation="MGOPGNGSAFLLAPNRSHAPDHDVTGQRDEVWVVGMHIVMSLIV
/translation="MGOPGNGSAFLLAPNRSHAPVGSLATWKARVILLAWMIV
/INVERTION LOTALING LATER LAT
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/gene="ADRB2"
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/gene="ADRB2"
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                                                                                                                                                                                                      http://webace.sanger.ac.uk/cgi-
bin/display?db-wormace&class-Sequence &object=Y17G7B
bin/display?db-wormace&class-Sequence &object=Y17G7B
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
overlap between neighbouring submissions.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
                                                             neighbouring submissions.

The true right end of clone W03C9 is at 100 in this sequence. The true right end of clone Y17G7 is at 143092 in this sequence. The true right end of clone Y17G7 is at 143092 with the end of sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (09-JUN-1998) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RO, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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1;283(5398):35 and 1999 Mar 26;283(5410):2103 and 1999 Sep
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end of this sequence (142993. .143092) overlaps with the start
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/chromosome="II"
/clone="Y38G4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                               Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of sequence ALI17199
                                                                                                       join(11683..11753,11836..11928,11980..12304,13242..1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(11683. 11753,11836. .11928,11980. .12304,13242. .1
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19438. .19658)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVSKGTWYFEVNFDDQPDDSHIRIGWSQSYASLQACVGYNKFSYGWRSKHGTKFHEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRGASKRRHAEAPYTGKKOKLAADYSSTAAPNGVQIDIPFSKDNYRYYLTEVDPNVPE
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KNIFVQHNDDDDLFALAEKNLSLLGPLHEAVKLIGKRPIERENRHPRHIELPPIEGPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SPTREMBL:Q9XXJ2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA19448.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3569. .4874)
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ANYFFEVQEESADIAKTLVEMPGSYIEFFHNGKSCGKAYENIYAGAYYPSISIFKSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKFRNLPRGATGIHARADEQQHEQTLSDMLYLVSKEVNLDHPPRVKREDDDDVKDIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                jóin(11683..11753,11836..11928,11974..12304,13242..1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="Y17G7B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Caenorhabditis elegans"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="cDNA EST EMBL:D35727 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to Acyl CoA binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L. .14309
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CDS

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Awnonossayyipsfhyrellnptvnyssndaafglsingnstigfegysmarashgv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYHFGGFKQGDVLGCLIHLPVDKKLQIPANLPSEKYLPVSHKGFNLISFKANYFFEVQ
EESADIAKTLVEMPGSYIEFFHNGKSCGKAYENIYAGAYYPSISIFKSATATMNLGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="myyvksllrradnemyivkkssearaallvdlyneedykeladk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="x17G7B.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28869
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yk535a10.3 comes from this gene; cDNA EST yk539f8.3 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Y17G7B.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="similar to Metallo-beta-lactamase superfamily"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(32881. .33253,34402. .35645,36629. .37493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Y17G7B.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oin(24223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .37816)
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gene CDS

gene

FEATURES

Exon/Intron boundaries of identified were canonical splice junctions that across the splice junctions.

Location/Qualifiers

genes were maintained

chosen if there sequence continuity

/organism="Homo sapiens"

.144368

The repeat regions shown were identified using RepeatMasker by

Sequence similarities were identified using Powerblast by Jinghui

source

CDS

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VERSION
KEYWORDS
SOURCE
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AC004103/c
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (17-APR-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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On Apr 18, 1998 this sequence version replaced gi:3056889.
Sequencing is completed to a minimum standard of double strand sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
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On Apr 18, 199
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join(52521. .52555,53285. .5
54595. .54744,54795<sub>.</sub> .54875)
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complement(8269. 8773)
/rpt_family="Lime1"
8878. .9769
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complement(10741. .10770)
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complement(12086. .12112)
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complement(21455. .22132)
/rpt_family="L1ME3A"
complement(22671. .22766)
/rpt_family="TIGGER2"
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6517.
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complement(2262. .2536)
/rpt_family="LTR16C"
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complement(843. .1139)
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                                                                                                                                                                 complement(17077. .17123)
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complement(18203. .18230)
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complement(14324. .14807)
/note="Region: Similar to gb:x69391 60S ribosomal protein
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complement(3366. .3465)
/rpt_family="L2"
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complement(19499. .19645)
/rpt_family="L2"
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/chromosome="x"
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/rpt_family="MIR"
3178. .31867
/rpt_family="MIR"
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/rpt_family="HERVH"
complement(33723...33983)
/rpt_family="HERVH"
complement(33974...34568)
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complement(23230. .23597)
/rpt_family="TIGGER2"
23587. .23655
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/rpt_family="AT_rich"
complement(42789. .42867)
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/rpt_family="HERVH"
complement(35229. .37784)
/rpt_family="HERVH"
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/rpt_family="FLAM_A"
44447. .44480
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complement/"
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/rpt_fam1ly="MER5A"
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/rpt_family="MSTB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(38041. .38170)
/rpt_family="LTR7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="LTR7"
complement/200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="HERVH"
complement/21555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="MSTB"
complement/complement/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt
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                                                                         /rpt_family="MLT1A1"
complement/54502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family-"MER8"
                                                                                                                                                                                                                                                                                                      /rpt_family='
                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_family-"L1MB8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="MSTB-internal"
                                                                                                                                                                                                                rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _family="MER34"
lement/2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _family="MER5A"
lement/30617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _family-
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                            Length 144368;
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SOURCE

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SOURCE
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CNS01RID
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                                                                                                                                                                                                                           BASE COUNT
ORIGIN
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                                                                                                   Matches
  59916 CAATAGAAGCCATGC 59930
                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                          1 caatagaagccatgc 15
                                                                                                                                                                                                                                                                                                                                                                                                                                               * by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 12418: contig of 12418 bp in length

* 12419 13418: gap of 1000 bp

* 13419 21210: contig of 7792 bp in length

* 21211 22210: gap of 1000 bp

* 22211 116554: contig of 93944 bp in length

* 116155 117154: gap of 1000 bp

* 117155 142308: contig of 25154 bp in length

* 142309 143308: gap of 1000 bp

* 143309 164162: contig of 20854 bp in length

* 143309 164162: contig of 20854 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (04-APR-2000) to the EMBL/GenBank/DDBJ databases IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.col1, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phage, etc.
Contig order: 6 5 9 7 8, 1000 N's separate segments Contig 6:
Length 12418 bp
Contig 5: Length 7792 bp
Contig 9: Length 93944 bp
Contig 7: Length 25154 bp
Contig 7: Length 25154 bp
Contig 8: Length 20854 bpX
Contig 8: Length 20854 bpX
Contig 8: Length 20854 bpX
Contig: This is a 'working draft' sequence. It currently
* NOTE: This is a 'working draft' sequence of the pieces
* are represented as runs of N. The order of the pieces
* are represented as runs of N. The order of the pieces
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HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSO1RID 164162 bp DNA
HTG 04-APR-200
Homo sapiens chromosome 14 clone R-98N22, *** SEQUENCING IN
PROCRESS ***, 5 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                     15;
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                                                                                                     Similarity 100
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                            /clone="R-98N22"
29753 c 28500
                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-11"
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                                                                                                        0;
                                                                                                   Score 15; DB 40;
Pred. No. 1.7e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                 4006 others
                                                                                                                                                           Length 164162;
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                                                                                                                   Gaps
                                                                                                                   0;
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RESULT

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HOMO Sapiens clone RP11-600K3, WORKING DRAFT SEQUENCE, 21 unordered
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Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 3200 this sequence version replaced gi:7249305. On Apr 3, 2000 this sequence version replaced gi:7249305. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                         * NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: L6507

Center clone name: 600 k.3

Center clone name: 600 k.3

Sequencing vector: M13; M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 184061 bases at least 040 consensus quality: 184061 bases at least Q30 consensus quality: 193764 bases at least Q30 consensus quality: 193765 bases at least Q20 insert size: 200000; agarose-fp

Insert size: 195540; sum-of-contigs
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 4.3 in Q20 bases; Quality coverage: 4.4 in Q20 bases;
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1308: contig of 1308 bp in length
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sum-of-contigs
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37846 46693: contig of 8848 bp in length
46694 46793: gap of 100 bp
46794 53246: contig of 6453 bp in length
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37846. .46693
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27631. .33314
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22644. .27530
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12250. 15980
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33415. .37745
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8681: gap of 100 bp
12149: contig of 3468 bp in length
12249: gap of 100 bp
15980: contig of 3731 bp in length
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                                                                                                                                                                                                                           Submitted (03 DEC-1998) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu on Aug 4, 1998 this sequence version replaced gi:2546913. Order of segments is not known; 800 n's separate segments. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
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* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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                                                /organism="Caenorhabditis
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On Mar 31, 2000 this sequence version replaced gi:7362707.
IMPORTANT: This sequence is unfinished and does not necessarily
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Contig_ID: 01027 Length: 3586bp
Contig_ID: 01061 Length: 4573bp
Contig_ID: 01066 Length: 4573bp
Contig_ID: 011086 Length: 4972bp
Contig_ID: 01113 Length: 2372bp
Contig_ID: 01126 Length: 8035bp
Contig_ID: 01215 Length: 1033bp
Contig_ID: 01218 Length: 1740bp
Contig_ID: 01252 Length: 1742bp
Contig_ID: 01252 Length: 1742bp
Contig_ID: 01252 Length: 1742bp
Contig_ID: 01252 Length: 182bp

* consists of 48 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                           102687 103486:
103487 113064
113065 113864:
113065 127227
113865 127227
127228 128027:
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64624 65423: gap of 65424 66729: contig of 1
66730 67529: gap of 80
67530 77646: contig of 3
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77599 8651
                             145278 146077:
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93245 94710: contig of 1466 l
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54704 56636: contig of 1933 k
56637 57436: gap of 800 bp
57437 58475: contig of 1039 k
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44510 51617: contig of
51618 52417: gap of
52418 53903: contig of
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61359: contig of 2084 b
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39771: contig of
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41584: contig of 1013 b
2384: gap of 800 bp
43709: contig of 1325 t
        18027: gap of 800 bp
145277: contig of 17250
16077: gap of 800 bp
148193: contig of 2116 b
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113064: contig of 9578 bp
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102686: contig of 7176 k
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27227: contig of 13363
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86515: contig of
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6280: contig of 4239 bp in length
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15; Conserva
Eukaryota; Metazos; Chordata; Craniata; Vertebrata; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1286) Rupert, J. L. and Hochachka, P. W. Beta-2-adrenergic receptor allele frequencies in two native
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165455 168028: contig of 2574 bp in length
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164654: contig of 8692
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208125: cont
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2 (bases 1 to 1286)
Rupert, J.L. and Hocha
Direct Submission
                                                                                                                                                                                                                                   l (bases 1 to 865)
Delectise, A. Bourgouin, C., Kiler, A. and Rapoport, G.
Nucleotide sequence and characterization of a new insertion
element, IS240 from Bacillus thuringlensis israelensis
Plasmid 21, 71-78 (1989)
                                                                                                                                                                                                                                                                                                                           Bacillus thuringiensis
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus
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B.thuringiensis insertion
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M23740.1 GI:
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                                                                                                                                                                                                                                                                                                                                                                                                                           insertion sequence.
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LAIVEGNVLVITAIAKEELLQTVTNYEITSLACADLYMGLAVVEPGAAHILMKMMTFQ
NEWCEFWTSIDVLCVYASIETLCVIAVDRY FAITSPFKYOSLLTKNKARVIILMVWIY
SGLTSFLPIQMHWYRATHQEAINCYANETCCDFFTNQAYAIASSIVSFYVPLVIMVFV
YSRVFQFAKRQLGKIDKSEGRRHVQNLSQVEQDGFTBGLTRSSKFCLKEHKALKTLG
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                                                         /note="left inverted repeat"
94. .801
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/product="beta-2 andrenergic receptor"
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/note-"IS240-A protein"
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                                                                                                         /organism~"Bacillus thuringiensis"
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/db_xref="taxon:9606"
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Pred. No. 3.6e+02;
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hes 14; Conservative
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300 a 143 c 176 g 246 t
53 bp upstream of Ball Site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Delecluse, A., Bourgouin, C., Klier, A. and Rapoport, G. Nucleotide sequence and characterization of a new insertion element, IS240 from Bacillus thuringiensis israelensis plasmid 21, 71-78 (1989) 89265213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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2 of 2
B.thuringiensis israelensis (strain 4Q2-72) DNA, clone pRX70.
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M23741.1 GI:
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B.thuringiensis insertion element IS240-B protein gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Draft entry and computer-readable sequence for
by A.Delecluse, 04-APR-1989.
Location/Qualifiers
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302 a 141 c 178 g 244 t
About 13.5 kb after segment 1; 53 bp upstream of Ball site
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ilarity 100.0%; Pred. No. 8.4e+02;
Conservative 0; Mismatches 0;
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/db_xref="G::143113"
/db_xref="G::143113"
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LDFYLSKKRDAKAKCFLKKALASFHYTKPRVITVDGNKAYPYAIRELKNEKSLPYGM
PLRVKKYLNNMIEQDHRFIKKRILNMLGLKSMQTAVKMIAGIEAMHMVKKGQLKLRAQ
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850.864
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PLRYKKYLMMIEQDHRFIKKRIRNMIGLKSMQTAVKMIAGIEAMHMVKKGQLKLRAQ
SAQNONRCIHQLFGLTA"
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HIV-2 variant HIV-
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ALIGNMENTS

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   WO9735963-A1.
02-OCT-1997; J00982,
24-MAR-1996; JP-072914.
(DAIN ) DAINIPPON PHARM CO LTD.
(UDAIN ) FUTUTANI Y, KAWASHIMA H
WPI; 97-489627/45.
P-PSDB; W34320,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel beta-2 adrenalin receptor sub-type - useful for screening for agonists and antagonists and researching asthmatic diseases Disclosure; Page 27-30; 47pp; Japanese.
This sequence encodes the protein of the invention is a beta-2 adrenalin receptor subtype with Kd value of approximately 75 pM against 1251-cyanopindrol. The protein can be used in screening for agonists and antagonists, which are useful in researching asthmatic diseases.

Sequence 1999 BP; 477 A; 513 C; 485 G; 524 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta-2 adrenalin receptor subtype coding sequence. Beta-2 adrenalin subtype; cyanopindrol; agonist; asthmatic disease; ss.
                                                                                                                                                   V52614 standard; cDNA; 3451 BP.
V52614;
V52614;
21-DEC-1998 (first entry)
Human beta-2-adrenergic receptor cDNA.
Beta-2-adrenergic receptor; human; asthma; beta-agonist;
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                                                                                                                     polymorphism; ds. Homo sapiens.
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231 CAATAGAAGCCATGC 245
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"A to G substitution, results to Gly amino acid change"
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pr Diagnosing asthma patients predisposed to adverse beta-agonist preactions upon regular administration - by identifying patients protections upon regular administration - by identifying patients protection protection beta2-adrenergic receptor protein Disclosure; Page 33-35; 46pp; English.

PS Disclosure; Page 33-35; 46pp; English.

PS Disclosure; Page 33-35; 46pp; English.

PS CC (CC This cDNA sequence codes for human beta-2-adrenergic receptor seek to comprises; (a) identifying an arginine residue at position 16. A novel method cc disclosure; Page 33-45; 46pp; English to adverse responses to comparise to the deta 2-adrenergic receptor gene, and (b) cc classifying an individual as susceptible if first and second cc alleles both encode Arg at residue 16 of the beta 2-adrenergic receptor gene alleles may be condition of the seta 2-adrenergic receptor gene alleles may be condition (see also v52615-17). Identification of PCR amplification (see also v52615-17). Identification cc comprises determining nucleotide sequences of these portions (e.g. cnounted sequence encoding residue 16, and optionally also cc comprises determining nucleotide sequences of these portions (e.g. by automated sequence analysis). The invention identifies a known cc polymorphism in the beta 2-adrenergic receptor gene as being linked to adverse responses to regular beta-agonist administration; condition is of the encoded protein can be either Arg or Gly, and conditional bomozygous for Arg16 are more susceptible.
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Q70084
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              Query Match
Best Local
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Transcriptional Court Transcriptions thuringiensis insecticidal proteins Claim 1; Page 7; 9pp; Japanese. Q70084 is a transcriptional control sequence isolated from Bacillus Q70084 is a transcriptional control sequence isolated for the expression of Bacillus thuringiensis insecticidal proteins. The isolation of this sequence allows the development of a host vector system in Bacillus thuringiensis and creation of highly insecticidal strains. The new strains created in this way are not recombinants, the insecticidal proteins produced using Bt as a host can be applied in agriculture.
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11-SEP-1998: U03908.
26-FEB-1998; U03908.
03-MAR-1997; US-811441.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
BOUShey H, Chinchilli VM, Drazen J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 98-506372/43.
P-PSDB; W75777.
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                                                                                                                                                                                                                          (SUMO ) SUMITOMO CHEM CO LTD. WPI; 94-275520/34.
                                                                                                                                                                                                                                                                                                                        Bacillus thuringiensis J06205682-A.
                                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis transcriptional control transcriptional control sequence; expression; Bacillus thuringiensis israelensis; develop; Insecticidal strain; ds.
                                                                                                                                                                                                          Transcriptional control sequence
                                                                                                                                                                                                                                                                   25-FEB-1992; 037748.
25-FEB-1992; JP-037748.
                                                                                                                                                                                                                                                                                                                                                                                                                                           04-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q70084 standard; DNA;
                                                                                                                                                                                                                                                                                                       26-JUL-1994.
                                                                                                                                                                                                                                                                                                                                                                insecticidal strain;
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29 CAATAGAAGCCATGC 1643
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l sequence; expression; insecticidal protein;
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Pred. No.
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                                                                                                                                                                                                              for the expression of Bacillus
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 EP-296870-A.
28-DEC-1988.
24-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  see also
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Ellar DJ, Ward ES;
WPI; 89-001322/01.
P-PSDB; P94035.
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28-DEC-1988.
24-JUN-1988; 305772.
26-JUN-1987; US-067653.
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                                                                                                                                                 misc_feature
                                                                                                                                                                                                        biological control agent
                                                                                                                                                                                                                              Delta-endotoxin;
                                                                                                                                                                                                                                          Delta-endotoxin crystal
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                                                                                                                                                                                     Bacillus thurigiensis subsp israelensis
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nilarity 100.0%;
Conservative
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/label=Shine-Delgarno sequence
                                                                                            /product=delta-endotoxin crystal protein RBS 879. 884
                                                                                                                                                     891. .4430
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No.
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Matches 14
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Best Local Similarity 100
Matches 14; Conservative
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N81490;
05-NOV-1990
Insecticidal
Insecticidal
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Ellar [
WPI; 89
                                                                                                                                                                                                                                                                                                   protein IG.
The insecticidal protein is commence 4934 BP; 1797 /
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Bacillus thuringiensis israelensis.
Koy
  X14561 standard; DNA; 1627
X14561;
31-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure: ; 9pp; Japanese.
A plasmid contg. the gene is isolated by forming from plasmid DNA of B.thuringiensis israelensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; P81034, P82589.

New insecticidal protein of Bacil

- propd. by forming gene library
gene, and transforming host cell.
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P-PSDB; P93715.
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19-MAR-1987;
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JP-066844.
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G; 1511 T;
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PD 08-OCT-1998.

PF 01-APR-1998; U06371.

PF 01-APR-1998; U06371.

PR 29-UUL-1997; US-902615.

PR 29-UUL-1997; US-833457.

PR 24-UN-1997; US-833457.

PR 24-UN-1997; US-832457.

PR 24-UN-1997; US-832457.

PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.

PI Al-Garawi A, Kleanthous H, Miller C, Oomen RP, Tomb J;

PR 40-1997; US-8329346

PR PSDB; W98842.

PR New isolated Helicobacter polynucleotides - used to develop products profort the diagnosis, prevention and treatment of Helicobacter references a polynucleotide of the invention. It was claim 1; Page 1884-1887; 2054pp; English.

CC This sequence represents a polynucleotide of the invention. It was claim 1; Page 1884-1887; 2054pp; English.

CC This sequence represents a polynucleotide of the invention. It was claim 1; Page 1884-1887; 2054pp; English.

CC This sequence represents a polynucleotide of the invention. It was claim 1; Page 1884-1887; 2054pp; English.

CC This sequence represents a polynucleotide of the invention. It was claim 1; Page 1884-1887; 2054pp; English, end encodes a H.pylori GHPO protein.

CC The polypeptides can be used for preventing or treating Helicobacter of infections, including acute, chronic, and atrophic gastritis, and peptic claim 1; Page 1884-1887; and peptic claim 1; Pag
 Query Match
Best Local S
Matches 14
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peptic ulcer disease; ss.
Helicobacter pylori.
                                                                                                                                                                                                                          26-APR-1991; 097697.
26-APR-1991; JP-097697.
(TAKS ) TAKASAGO PERFUMERY CO LTD.
WPI; 93-003497/01.
New phenylalanine ammonia lyase genuplasmid contg: gene, and E. coli tr
                                                                                                                                       prepn. of lyase.
Disclosure; Page 8; 9pp; Japanese.
The sequence is that of the phenylalanine from Pisum sativum L. The gene may be use recombinantly. Plants contg. the PAL gene
                                                                                      of phenyl propanoid
See also Q31985.
Sequence 1707 BP;
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18-NOV-1992.
                                                                                                                                                                                                                                                                                                                                                                            Pisum sativum.
                                                                                                                                                                                                                                                                                                                                                                                             pea; ss
                                                                                                                                                                                                                                                                                                                                                                                                           Phenylalanine
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a lyase;
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93.3%;
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E. coli transformed with plasmid,
Score 13.4; D
Pred. No. 96;
O; Mismatches
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Pred. No. 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            the S.aureus DNA sequences allows putative functions to be assigned so that protein encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-S.aureus vaccines
Claim 1; Page 1956; 3271pp; English.
This sequence represents one of 5191 Staphylococcus aureus DNA sequences
of the invention. The DNA sequences are recorded on a computer readable
medium, preferably selected from a floppy or hard disk, random access
memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus contig SEQ ID #1435.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelld infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                       DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                  computer
Sequence
W09730070-A1
                                           Staphylococcus
Key
                                                                            vaccine; Staphylococcal i
toxic shock syndrome; ss.
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07-JAN-1997; 100117.
05-JAN-1996; US-009861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   toxic shock syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V75746
                                                                                                                                                                           T83720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide(s) and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 97-374922/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                           l6-JUL-1998 (first entry)
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nes 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                   readable medium.
116 BP; 38 A;
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                               aureus
                              complement (44. .415)
                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                      86.7%;
100.0%;
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                                                                                           infection; food poisoning;
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scaled skin syndrome;
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Query Match Best Local Matches

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86.7%; 100.0%;

Score 13; Pred. No.

DB 1; 1.4e+02;

Length 521

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05-JUN-1995; 463115.
05-JUN-1995; US-463115.
05-JUN-1995; US-763115.
23-MAY-1991; US-763039.
20-SEP-1991; US-763039.
22-MAY-1992; US-887502.
23-NOV-1993; US-157811.
Stealth virus nucleic acid molecule - useful to detecting stealth virus, e.g. in chronic fatigue syndrome diagnosis

Example 5; Fig 1; 82pp; English.

V10141-V10210 represent nucleic acid sequences obtained from a patient with a stealth virus infection, namely chronic fatigue syndrome (CFS). Such nucleic acid sequences can be used to detect the stealth virus in medical, veterinary and agricultural diagnostics and in industrial and pharmaceutical biological quality control, e.g. to diagnose a disease associated with the stealth virus.

Sequence 521 BP; 119 A; 146 C; 117 G; 105 T;
                                                                                                                                                                             Martin WJ;
WPI; 98-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.

Sequence 417 BP; 134 A; 66 C; 78 G; 132 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 638; 989pp; English.

The present sequence encodes a Staphylococcus aureus protein unknown function. The present sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. I sequence can be used in the construction of ribozymes and ant sequences to control the expression of Staphylococcal genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-1997.
19-FEB-1997; U02318.
20-FEB-1996; US-011888.
(SMIK ) SMITHKLINE BEECHAM CORP.
Black MT, Burnham MK, Hodgson JE, Kr
                                                                                                                                                                                                                                                                                                                                                                                               29-MAY-1998 (first entry)
Stealth virus nucleic acid in plasmid #4.
Stealth virus; chronic fatigue syndrome; CFS; disease; detection; medical diagnostic; veterinary diagnostic; agricultural diagnostic;
                                                                                                                                                                                                                                                                                                                                                 US5703221-A.
                                                                                                                                                                                                                                                                                                                                                                    Stealth
                                                                                                                                                                                                                                                                                                                                                                                 quality control; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The encoded protein may be us to produce vaccines to enable a host to produce specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptide(s) from Staphylococcus to isolate antimicrobial compounds, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                MARTIN W J.
                                                                                                                                                                                                                                                                                                                                                                  virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Knowles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aureus strain WCUH29 in vaccines against S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
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S

caatagaagccat 13

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VILLA RESULT
VILLA
    760570, TR60570, TR60
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Best Local S
Matches 13
                                                                                                          J09075093-A.
25-MAR-1997;
20-FEB-1996; 031987.
21-FEB-1995; US-391696.
29-DEC-1995; US-580545.
(TOYM) TOYOBO KK.
(UYTE-) UNIV TEXAS TECH.
WPI; 97-239274/22.
P-PSDB; W15762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAY-1998.

05-JUN-1995; 465388.

05-JUN-1995; US-465388.

23-MAY-1991; US-704814.

20-SEP-1991; US-763039.

22-MAY-1992; US-887502.

23-NOV-1993; US-157811.

(MART/) MARTIN W J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 98-31405/27.

WPI; 98-31405/27.

WPI; 98-31405/27.

Stealth virus contained in MRC-5 cell line, ATCC number VR2343 - is useful as a vaccine against chronic fatigue syndrome Disclosure; Fig 1A; 99pp; English.

V11954-V12024 are plasmids which contain fragments of a stealth virus isolated from a patient, D.W. Such stealth virus fragments can be used as vaccine against chronic fatigue syndrome (CFS). This illness causes unexplained fatigue lasting more than 6 months and greater then 50% reduction in an infected persons normal level of activity. The virus causes a cytopathic effect (CPE) to fibroblast cells observed in culture, characterised by the appearance of rounded, slightly enlarged, refractile cells in the culture.

Sequence 521 BP; 119 A; 146 C; 117 G; 105 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cotton fibrous tissue specific gene Gh2.
Fibrous tissue; cotton fibre; cotton flc
Gossypium hirsutum; 88.
Gossypium hirsutum; 88.
Key
Gossypium hirsutum.
Key
37. 447
Cotton fibrous tissue gene - used to improved cotton fibres, and improved Claim 2; Page 22-23; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-1998 (first entry)
Stealth virus plasmid 4 DNA.
Chronic fatigue syndrome; CFS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T60570 standard;
T60570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5753488-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Martin WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stealth virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V11957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V11957 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CANTAGAAGCCAT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag- a
/product- fibrous tissue specific protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA; 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13; DB 1; L4; Pred. No. 1.4e+02; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; cytopathic effect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                          produce transformants with yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 flower;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gossypium barbadense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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RESULT 1
V37345/c
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                                                                                                                  Sclaim 1; Page 47; 130pp; English.

Strike sequence is that of a coding region isolated from S. pneumoniae. Its encoded protein, or agonists of it, may be useful as an antibacterial for treatment or prevention of infection, specifically caused by S. pneumoniae (particularly meningitis) but possibly also Helicobacter pylori (ulcers and gastric cancer). It may be of particular use before insertion of an in-dwelling device or any other invasive procedure. The protein, or nucleic acid encoding it, can also be used in vaccines to induce a cellular and/or humoral immune response, or to screen for other that are potential sources of control elements for bacterial gene expression. Detecting a sequence encoding the protein can be used diagnostically, egents.

Sequence 740 BP; 266 A; 141 C; 160 G; 173 T;
                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM C

(SMIK ) SMITHKLINE BEECHAM P

Black MT, Hodgson JE, Knowle

Reid RH, Zarfos PN;

WPI; 98-286586/25.

P-PSDB; W60945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  760567-T60571 represent cotton fibrous tissue genes of the invention. These sequences are specifically expressed during the growth of cotton fibre. The genes were isolated from the polya RNA of the ovules of a cotton flower of Gossypium barbadense, and G. hirsutum. These sequences, and vectors containing them are used in the preparation of cotton transformants, with improved cotton fibres and improved yield. Sequence 713 BP; 200 A; 131 C; 161 G; 221 T;
                                                                                                                                                                                                                                                                                                                                                  e.g. for identifying anti-bacterial(s) for treatment and of meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-1997; U19226.
01-NOV-1996; US-029930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae coding region; ORF; open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9819689-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V37345 standard;
356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 caatagaagccat 13
                        1 caatagaagccat 13
CAATAGAAGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAATAGAAGCCAT
                                                 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or, open reading frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (1. .261)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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344
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100.0%;
                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitis; ss.
                                                                 .08;
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                                                                Score
Pred.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       frame; antibacterial;
                                                                . 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Lonetto MA, Nicholas
                                               DB 1; LC. 1.5e+02; 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; L
1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                             Length 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                    pneumoniae
                                                                                                                                                                                                                                                                                                                                                                    prevention
                                                                                                                                                                                                                                                                                                                                                                                  useful,
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                                                    Gaps
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                                                    0
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DY 972393/6

DY 97239;

AC 479239;

DY 16-MAR-1999 (first entry)

DE Staphylococcus aureus contig SEDO ID #928.

WY Computer readable medium; vaccine; S.aureus infection; immunodetection;

WW computer readable medium; vaccine; S.aureus infection; immunodetection;

WW computer readable medium; vaccine; S.aureus infection; sended skin syndrome;

WW callulitis; eyelid infection; rood poisoning; ostcomyelitis; therapy;

WW skin infection; surgical wound infection; scalded skin syndrome;

WW collulitis; eyelid infection; cond infection; scalded skin syndrome;

WW collulitis; eyelid infection; scalded skin syndrome;

PR 20-74M-1997; 100117.

PR 05-74M-1997; 100117.

PR 05-74M-1997; 100117.

PR 05-74M-1997; 100117.

PR 107-84M-1997; 1
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90.:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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        112.44
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Match Length DB
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15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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521
713
1863
2121
2121
3592
33
54
                                                         6 PCT-US91-00909-3
4 US-08-63-3-879C-17
4 US-08-963-743-7
1 US-08-095-726-19
1 US-08-095-726-19
1 US-08-095-623-24
1 US-08-096-623-24
2 US-08-463-115-10
2 US-08-463-115-10
2 US-08-463-381-7
1 US-08-126-646-1
1 US-08-133-879C-17
1 US-08-133-879C-17
3 US-08-133-240A-1105
1 US-08-363-240A-1105
1 US-08-363-240A-1105
1 US-08-363-240A-1105
1 US-08-363-240A-1105
1 US-08-08-11-177A-3
1 US-08-08-11-177A-3
1 US-08-08-11-177A-1
1 US-08-08-726A-63
1 US-08-08-726A-63
1 US-08-08-726A-63
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Sequence 3, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 10, Appli
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Sequence 1055, Appli
Sequence 1141, Appli
Sequence 11, Appli
Sequence 67, Appli
Sequence 67, Appli
Sequence 64, Appli
Sequence 67, Appli
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    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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Result No.

0000 0 00

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Score 15; DB 6 Pred. No. 7.6; 0; Mismatches

DB 6; Length 1242; Indels

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C 45	C 44	C 43	c 42	41	c 40	c 39		37	36	35	34	33	32	31	30	29	28	
12	12	12	12	12	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	
80.0	80.0	80.0	80.0	80.0	82.7	82.7	82.7	82.7	82.7	82.7	82.7	82.7	82.7	82.7	82.7	82.7	82.7	
450	450	450	68	40	15328	15328	12047	7493	7493	7493	7493	4060	4060	4060	4060	4060	4060	
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JS-08-596-024-4	JS-08-398-627-28	US-08-090-523-28	US-08-776-900C-40	US-08-443-957-18	°CT-US94-07926-33	US-08-888-497-33	US-09-022-461-1	PCT-US94-13200-5	US-08-670-707A-5	US-08-474-503-5	US-08-212-133A-7	US-08-845-623-7	US-08-845-623-5	US-08-845-623-3	US-08-845-623-1	US-08-164-292B-7	US-08-164-292B-5	CC
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Codecico
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4, Appli	Appl	Appl	App1	App1	Appl	App1	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appl1	Appli	44.4

ALIGNMENTS

PCT-US91-00909-3 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-622-4900 TELEFAX: 206-682-6031 TELEX: 3723836 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1242 base pairs Sequence 3, Application PC/TUS9100909 GENERAL INFORMATION: APPLICATION NUMBER: PCT/US91/ FILING DATE: 19910208 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: MAK1, Dav1d J. REGISTRATION NUMBER: 31,392 REFERENCE/DOCKET NUMBER: 9900 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICANT: Sledziewski, Andrzej z. APPLICANT: Sheppard, Paul O. APPLICANT: Sheppard, Paul O. TITLE OF INVENTION: Methods of Producing Hybrid G TITLE OF INVENTION: Protein-Coupled Receptors STRANDEDNESS: sin TOPOLOGY: linear MOLECULE TYPE: cDNA FEATURE: NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: NAME/KEY: LOCATION: COUNTRY: United States ZIP: 98104-7092 CITY: Seattle STATE: Washington TYPE: NUCLEIC ACID ADDRESSEE: 6300 Columbia Center, 701 Fifth Ave Seed and Berry single PCT/US91/00909 990008.408PC

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               RESULT 3
US-08-963-743-7
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                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPAX: 650-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/08633879C Patent No. 5928922
Sequence 7, Application US/08963743
                                                                                                                                                    Matches
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Niss1, KILVA N.
APPLICANT: No. 5928922elainen, Minna K.
TITLE OF INVENTION: '2 SUBUNIT OF PROLYL-4-HYDROXYLASE'
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING SUCH SUBUNIT AND TITLE OF INVENTION: METHODS FOR PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                    OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2121 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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| 12 CAATAGAAGCCATGC 56
                                                                                                                                                                                                                                                   NAME/KEY: Coding Sequence LOCATION: 96...272
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08 FILING DATE: 10-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                    Local Similarity
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1155 Avenue of the Americas
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Helaakoski, Tarja I.
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                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                    93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8389-0041-999
                                                                                                                                                    Mismatches
                                                                                                                                                                    DB 4;
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                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 472-9650
TELEPAX: (970) 472-9655
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                             APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedh
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Huei-Che B
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APPLICANT: PALMER, Reid G.
APPLICANT: SHOWMAKER, Randy C.
APPLICANT: SOYDean Glucanases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/963,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 737 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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HYPOTHETICAL: NO
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                TITLE OF INVENTION: Beta-Caroten TITLE OF INVENTION: Genetically NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                 448 CAATAGCAGCCATGC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Kristine H. Joh
STREET: 123 No. 5952548th
CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: JOHNSON, Kristine H. REGISTRATION NUMBER: 36,835 REFERENCE/DOCKET NUMBER: P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                    ADDRESSEE: AND COMPANY 200 E Randolph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 80524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
STATE: IL
COUNTRY: USA
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14; Conservative
                               Chicago
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                                                                                                                                                                                              Brinkhaus, Friedhelm L
Mukharji, Indrani
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8th College Avenue,
                                                                 Patents
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Pred. No. 55;
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                                                                                                                Engineered
                                                                   and Licensing Dept
                                                                                                                                 Biosynthesis
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

60680-0703

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TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-095-726-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-096-043-16
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Best Local Similarity
Matches 13; Conserv
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Patent No. 5530189
GENERAL INFORMATION:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,043
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
CROSSIFICATION DATA:
APPLICATION NUMBER: US 07/785,568
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530189val B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PACENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/095,726
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/785,566
FILING DATE: 30-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530188val B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Lycopene Biosynthesis in TITLE OF INVENTION: Genetically Engineered Hosts NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                        STREET: 200 E
CITY: Chicago
STATE: IL
                                                                                                                                                                                                                                                                  STATE: IL COUNTRY: USA ZIP: 60680-0703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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200 E Randolph St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Proffitt, John H
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htive 0;
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-093-577-12
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                                TELEPAX: 3128564974
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/785,569
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5545816val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Phytoene Biosynthesis in TITLE OF INVENTION: Genetically Engineered Hosts NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yarger, James G
APPLICANT: Yen, Huel-Che B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 19-JUL-1993
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5545816
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200 E Randolph St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brinkhaus, Friedn
Mukharji, Indrani
Proffitt, John H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ausich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodney L
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Pred. No.
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Query Match

Best Local Similarity Matches 13; Conserv

Conservative

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Mismatches

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Indels

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Gaps

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86.7%; Score 13; DB 1; Length 39; 100.0%; Pred. No. 70;

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                                                 Query Match
Best Local :
                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                   TELEFAX: (312) 655-1501
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,613
FILING DATE: 02-MAR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Biosynthesis of Zeaxanthin and
TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 655-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                 Local Similarity
les 13; Conserv
                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 28-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 22-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
2 aatagaagccatg 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATAGAAGCCATG 21
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Yen, Huei-Che B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brinkhaus, Friedhelm
Mukharji, Indrani
Proffitt, John H. '
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ausich, Rodney L
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                                                                                                                                   DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                       Edward P.
                                             100.0%;
                                                 86.7%; Score 13; DB 1; 100.0%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 07/562,674
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                                                                                                                                                                                                                                                                                                                       29,381
                          0;
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                                 Mismatches
                                 0;
                                                                 Length 39;
                               Indels
                               0;
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; OTHER INFORMATION:
US-08-463-115-10
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US-08-463-115-10
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                                                                      Matches
                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/463,115
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: Including application partice of the prior application data: including application data: including application data: including application partice of the prior application number: 08/157,811
FILING DATE: No. 5703221ember 23, 1993
APPLICATION NUMBER: 07/887,502
FILING DATE: May 22, 1992
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
                                                                                                                                                                                                                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: September 20, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WILLIAM JOHN MARTIN
1 caatagaagccat 13
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218 CAATAGAAGCCAT 230
                                                                                                                                                                                                                        LENGTH: 521 base pairs TYPE: nucleic acid STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5" Di
                                                                                    Local Similarity
                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/763,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                               TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Lyon & Lyon 633 West Fifth Street Suite 4700
                                                                                                                                                                                                                                                                                                                                (213) 955-0440
                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM: IBM P.C. DOS 5.0 FastSeq Version 1.5
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100.0%; Pr
100.0%; 0;
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                                                                                                                                                                                                                                                                                                10:
                                                                                      Score 13; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                   213/301
                                                                      Mismatches
                                                                                      DB 2;
89;
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                                                                                                    Length 521;
                                                                      Indels
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RESULT 9 US-08-465-388-10

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sequence 10, Application US/08465388 Patent No. 5753488

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US-08-580-545B-7/c
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                                                                                                                                                                                             RESULT 10
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
                                       Sequence 7, Application US/08580545B Patent No. 5932713
GENERAL INFORMATION:
APPLICANT: YOShihisa, Kasukabe
APPLICANT: Kolchi, Fujisawa
APPLICANT: Susumu, Nishiguchi
APPLICANT: Yoshihiko, Maekawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/157,811

FILING DATE: No. 5753488ember 23, 1993

APPLICATION NUMBER: 07/887,502

FILING DATE: May 22, 1992

APPLICATION NUMBER: 07/704,814

FILING DATE: May 23, 1991

APPLICATION NUMBER: 07/763,039

FILING DATE: May 23, 1991

APPLICATION NUMBER: 07/763,039

FILING DATE: September 20, 1991

APPLICATION NUMBER: 07/763,039

FILING DATE: September 20, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENERAL INFORMATION:
APPLICANT: WILLIA
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APPLICATION NUMBER
FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 213/300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon 6 Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                  218 CAATAGAAGCCAT 230
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                      1 caatagaagccat 13
T: YOShihiko, Maekawa
T: Randy, Allen
INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WILLIAM JOHN MARTIN
VENTION: ISOLATED STEALTH VIRUSES
VENTION: AND RELATED VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
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100.0%; Pr
0;
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                                                                                                                                                                                                                                                                                                                                            Score 13; DB 2; Length 521; Pred. No. 89;
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RESULT 11
US-09-126-646-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 86.7%; Score 13; Best Local Similarity 100.0%; Pred. No. Matches 13; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: BRUN, KIMBERLY A.
APPLICANT: CREASY, CARETHA L.
APPLICANT: DUNNINGTON, DAMIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/783-5070
TELEFAX: 202/783-231
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bretschnelder, Barry E.
REGISTRATION NUMBER: 28,055
REGISTRATION NUMBER: 04473/068001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,646
FILING DATE: 31-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DUNNINGTON, DAMIEN J.
TITLE OF INVENTION: HUMAN PROTEIN KINASE H2LAU20
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: fish & Richardson P.C.
STREET: 601 Thirteenth Street, NW
                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 601 Thir CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                            STREET: P.O. Box 9t CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 19482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                STATE: PA
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 CAATAGAAGCCAT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 caatagaagccat 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09126646
                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                     Ratner & F
.O. Box 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                           & Prestia
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91;
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Prestia, Paul F

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Best Local Similarity
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                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NISSI, Ritva K.

APPLICANT: NO. 5928922elainen, Minna K.

TITLE OF INVENTION: '2 SUBUNIT OF PROLYL-4-HYDROXYLASE
TITLE OF INVENTION: NUCLEEIC ACID SEQUENCES ENCODING SUCH SUBUNIT AND
TITLE OF INVENTION: METHODS FOR PRODUCING THE SAME
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 610-407-0700
               SEQUENCE CHARACTERISTICS:
LENGTH: 2121 base pairs
TYPE: nucleic acid
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                             TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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TYPE: nucleic acid
STRANDEDNESS: single
                                                              TELEFAX: 650 TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/01 FILING DATE: 10-APR-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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LECOMMUNICATION TOTAL
                                                                                                                                               NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-0041-999
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
STRANDEDNESS:
                                                                                                                                                                                                                                    APPLICATION NUMBER:
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       610-407-0700
                                                                                               : 650-493-4935
650-493-5556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pihlajaniemi, Taina
Helaakoski, Tarja I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No.
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; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 96...272
; OTHER INFORMATION:
US-08-633-879C-17
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GENERAL INFORMATION:
APPLICANT: Maisonpierre, et al.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D., Gail M
REGISTRATION NUMBER: 32,143
REGISTRATION NUMBER: 32,143
REGISTRATION NUMBER: 32,143
                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Maisonpierre, et al.
TITLE OF INVENTION: EHK AND FOR TYROSINE
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3592 base pairs
                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: RETELECOMMUNICATION INFORMATION: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                   FEATURE:
                                                                                                                                   FEATURE:
                                                                                                                                                    MOLECULE TYPE:
                                              NAME/KEY:
LOCATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                LOCATION:
                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                    TYPE: nucleic acid STRANDEDNESS: unknown
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                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                    unknown
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100.0%;
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 /label= N
/note= "Where N = G,
                                  /mod_base= OTHER
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Pred. No.
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; HYPOTHETICAL: NO
US-08-836-402B-1
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Best Local Similarity lov.
3; Conservative
                                                           Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/836,402B
FILING DATE: 02-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 44 40 200.7 (Germany)
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: KUIT G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9840-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1836 AATAGAAGCCATG 1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Microsoft Windows 98
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rudiger Hain, Regina Fischer
TITLE OF INVENTION: DNA SEQUENCE AND ITS USE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 3538
OTHER INFORMATION: /mod_base- OTHER
OTHER INFORMATION: /label- N
OTHER INFORMATION: /note- "where N - G, A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Gateway 2000
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 660 White CITY: Tarrytown STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 10591-5144
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                 1 caatagaagccatg
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                                                                                                                                                                                                                                        33 base pairs
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified_base 3538
                                                                                                                                                                           DNA (genomic)
                             14
                                                                             82.7%;
92.9%;
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100.0%; Pred. No.
tive 0; Mismatc
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                                                           Score 12.4; DB 5;
Pred. No. 1.5e+02;
0; Mismatches 1;
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Search completed: September 12, Job time: 3946 sec
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US-08-363-240A-1055
                                                                                                                                                                                                                                                  ; TOPOLOGY: 1
US-08-363-240A-1055
                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEEAX: (213) 955-0440
TELEEX: 67-3510
INFORMATION FOR SEQ ID NO: 1055:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
                                                                                                                                                   Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Courses
APPLICANT: McSwiggen, James
APPLICANT: Bisgaler, Charles
APPLICANT: Pape, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bisgaier,
APPLICANT: Page, Mic
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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STREET: Suite 4700
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85.7%;
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                2000, 23:04:39
                                                                                                                                                                           Score 12.4; DB 2;
Pred. No. 1.5e+02;
                                                                                                                                                            Mismatches
                                                                                                                                                                                          Length 54;
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Title:
Perfect score:
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Maximum
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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seq length: 1000000
 September 12, 2000, 22:46:49; Search time 1893.64 Seconds (without alignments)
34.931 Million cell updates/sec
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        em_est1: *
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9b_est25:
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9b_gss6:
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RESULT
AW598789
LOCUS
                        DEFINITION
AW598789 287 bp mRNA EST 22-M
ga88b04.y1 Moss EST library PPU Physcomitrella patens
PEP_SOURCE_ID:PPU161308 5', mRNA sequence.
                              cDNA clone
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Local Similarity les 15; Conserv

Conservative

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Indels

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Gaps

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ALIGNMENTS

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        pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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AG317207 RPCI11-10
AG199592 RPCI11-14
BAG78011 HS_553LB
AG777734 HS_2190_B
AW674779 ba59e06.y
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AZ018937 RPCI-23-2
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AW067032 AV067032
AW16641 xm53b07.x
B68841 CIT-HSP-20
AA241735 JA00A074
AW488772 U1-W-BH3-AA8332805 uc92b01.r
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                     AA129379 zn85a08.s
AW457447 UI-M-BH3-
AW654359 103772 MA
AQ198499 RPCI11-62
AI468443 tg81d07.x
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AV132414 AV132414
                                                     W81900 me92c02.rl
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AZ008470 RPCI-23-2
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AW598789.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
On Jul 8, 1999 this sequence version replaced g1:5422558
Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
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Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
Libraries were constructed by Dr. Stavros Bashiardes as part of th
Libraries were constructed by Dr. Stavros Bashiardes as part of th
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
Colone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Seq primer: -40Rp from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Funariidae;
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Fax: 314 286 1810
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                                                                                                                                                                                                             /lab_host="DHIUB"
//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Constructed out
using Stratagenes 'UniZAP - cDNA synthesis kit'. cDNA
was constructed using an oligo dT primer/linker that
contains a XhoI site within it. Following ds cDNA
synthesis, EcoRI adapters were ligated to the blunt ends
and sample was digested with XhoI. The result is cDNA
and sample was digested with XhoI. The result is cDNA
with an EcoRI sticky end on one side and a XhoI sticky
end on the other. This cDNA was ligated directionally in
UnizAP arms. The vector is designed containing the
pBluescript sequence as well as lambda DNA and cDNA is
cloned within this pBluescript sequence. The vector was
cloned within this pBluescript sequence. The library
was grown in XLIBLUE MRF' cells and amplified. The library
was grown in XLIBLUE MRF' cells and amplified. The library
was excised by mass excision using Stratagens 'Mass
was excised by mass excision using Stratagens 'Mass
was excised by mass excision using Stratagens 'Mass
single stranded plasmids that are then packaged (by helper
phage) and secreted out of the host cell as phagemids.
SOLR cells were transformed with phagemids and the library
was plated out on LB-amp plates to select for
transformants, Approximately 1,000,000 colonies were grown
and recovered by using Quiagen Midi prep kit. 2 micro grams of
each library were used to transform DH10B cells by
electroporation."
61 a 69 c 74 g 83 t
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/clone_lib="Moss EST library PPU
/tissue_type="protonemata: 7 day
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/lab_host="DH10B"
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/db_xref="taxon:3218"
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           Score 15; DB 74; I
pred. No. 1.2e+02;
pred. No. 1.2e+02;
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M., Bowers,Y., Person,B.,
,, Harvey,N., Ritter,E.,
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72 AATAGAAGCCATGC 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV132414 219 bp mRNA EST 01-JUL-1999 AV132414 Mus musculus C57BL/6J 11-day embryo Mus musculus cDNA clone 2700089N23, mRNA sequence.
  AQ553837.1
GSS.
                                                             AQ553837 312 bp DNA RPCI-11-357N10.TJ RPCI-11 Homo sapiens 357N10, genomic survey sequence. AQ553837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. 95(2):50-524 (1956). Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998)) Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
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Unpublished (1999)
On Apr 7, 1998 this sequence version replaced g1:3035541.
Contact: Chie Owa
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 219)
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Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Science Laboratory
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/clone="2700089N23"
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59 c 50 g 28 t
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/strain="C57BL/6J"
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
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The Institute for Genomic Research
Unpublished (1999)
On Dec 15, 1999 this sequence version replaced gi:4574988.
Contact: Shaying Zhao
Department of Eukaryotic Genomics
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AZ008470
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                              Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., K
Jong, P. and and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
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Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 398)
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/db_xref="GDB:7637025"
/db_xref="taxon:9606"
/clone="RPCI-11-357N10"
/clone_lib="RPCI-11"
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/note="Vector: pBAC63.6; Site_1:
/note="Vector: pBAC63.6; Site_1:
/note="Vector: pBAC63.6; Site_1:
/note="Lymphocytes"
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Pred. No. 4.9e+02;
0; Mismatches 0;
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Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or fi
                                                                                                                                                                                                                                                                                               Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
Other_GSSs: RPCIII-106B3.TV
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GSS.
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                                                                                                                                                                                                                                                  Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
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                                                                                                                                               Tel: 301 838 0200
Fax: 301 838 0208
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-246M9"
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/sex="Female"
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RPCI11-48H5.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-
48H5, genomic survey semience
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are darived from the human BAC library RPCI-11. For BAC
Clones are darilability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
Other_GSSs: RPCI11-48H5.TK
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Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,F. and Venter,J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
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Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="RPCI-11-106B3"
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/sex="Male"
                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:7518220"
/db_xref="taxon:9606"
/clone="RPCI-11-48H5"
/clone_lib="RPCI-11"
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/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
RPCIll Human Male BAC Library"
85 c 112 g 70 t
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI;
RPCII1 Human Male BAC 1.brary"
84 c 95 g 130 t
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                                                                                     /sex="Male"
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2 aatagaagccatgc 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library avallability, please contact Pleter de Jong
(pletcr@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (Info@resgeh.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1107 row: N column: 14
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HS_5531_B2_G07_SP6E RPCI-11 Human Male BAC Library Homo
sapiens genomic clone Plate=1107 Col=14 Row=N, genomic survey
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Class: BAC ends
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ilarity 100.0%;
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                                                                                                                                                                           /note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

157 t 7 others
                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=1107 Co1-14 Row=N"
                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-11 Human Male BAC Library"/sex="male"
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                                                         93.3%; Score 14; DB 113;
100.0%; Pred. No. 5.3e+02;
tive 0; Mismatches 0;
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5.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2190 row: B column: 14
Seq primer: M13 Reverse
Class: BAC ends
                                                                                                   ;, mRNA sequence.
AW674779
                                                                                                                                   AW674779 515 bp mRNA EST 11-APR-20 ba59e6.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900866 similar to SW:SP49_HUMAN Q15427 SPLICEOSOME ASSOCIATED PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Sep 10, 1998 this sequence version replaced gi:3554391. Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington
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HS_2190_B2_A07_MR CIT Approved Human Genomic Sperm Library |
Homo sapiens genomic clone Plate=2190 Col=14 Row=B, genomic
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Location/Qualifiers
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
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E-Coli DH10B"
a 85 c 96 g 166 t 1 others
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/clone_11b="CIT Approved Human Genomic Sperm Library D"
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/db_xref="taxon:9606"
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On Jul 7, 1999 this sequence version replaced gi:5407333.
Other_ESTs: ba59e06.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 515)
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HS_5459_B2_D06_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1035 Col=12 Row=H, genomic survey
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 515) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Adams, M.D. ai
                                                                                                                                                                                                                                                                                                                                                                                       GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
                                                       On Dec 15, 1999 this sequence version replaced g1:4215181. Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington
401 Queen Anne Avenue North,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                          scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17),
                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to
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/db_xref="taxon:9606"
/clone="IhMAGE:2900866"
/clone=lib="NHH_MGC_10"
/cell_line="MGC36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.5 kb. Library prepared by Life Technologies."
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. 5.4e+02;
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                                                                                                                                                                                                           mapping
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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1035 row: H column: 12
Seg primer: T7
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   Quatrano, R., Bashiardes, S., Cove, D., Cuming, A., Knight, C., Clifton, S., Marra, M., Hiller, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R. Leeds, Wash U Moss EST Project
                                                                                                                                                                                                                                                                   Unpublished (1999)
On Jan 6, 2000 this sequence version replaced On Jan 6, 2000 this sequence version replaced Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Physcomitrella patens
Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
Funaridae; Funariales; Funariaceae; Physcomitrella.

1 (bases 1 to 519)
                                       Libraries were constructed by Dr. Stavros Bashiardes as part of the Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and Washington Univ. in St. Louis (USA) DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Celia Knight (c.d.knight@leeds.ac.uk) seq primer: -40RP from Gibco
                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                 Email: est@watson.wustl.edu
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                    quality sequence stop: 425
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wale blood DNA was isolated from one randomly chosen
and partially digested with a combination of EcoRI an
EcoRI Methylase. Size selected DNA was cloned into th
pBACe3.6 vector at EcoRI sites"
a 120 c 102 g 152 t 4 others
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/db_xref="taxon:9606"
/clone="plate=1035 Col=12 Row=H"
/clone_lib="RPCI-11 Human Male BAC Library"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                     AQ113165.1
GSS.
                                         Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                   Unpublished (1998)
Other_GSSs: CIT-HSP-237509.TR
                                                                                                                                                                                                                                         1 (bases 1 to 539)
Adams, M.D:, Rounsley, S.D., Zhe
Borry, K., Granger, D., Suh, E.,
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                             Use of a random human BAC
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14; Conservative
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Medical Center Dr., Rockville, 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Construction of the cDNA library was carried out using Stratagenes 'UniZAP - CDNA synthesis kit'. cDNA was constructed using an oligo dT primer/linker that contains a xhoI site within it. Following ds cDNA synthesis, EcoRI adapters were ligated to the blunt ends and sample was digested with xhoI. The result is cDNA with an EcoRI sticky end on one side and a xhoI sticky end on the other. This cDNA was ligated directionally in UniZAP arms. The vector is designed containing the pBluescript sequence. The vector was cloned within this pBluescript sequence. The vector was then packaged using Gold glgapackaging extracts. Library was grown in XLDBlue MRF' cells and amplified. The library was grown in XLDBlue MRF' cells and applified. The library was excised by mass excision using Stratagens 'Mass excision kit' that uses exassist as a helper phage that releases the pBluescript sequence and circularises it as single stranded plasmids that are then packaged (by helper phage) and secreted out of the host cell as phagemids. SOLR cells were transformed with phagemids and the library was plated out on LB-map plates to select for transformants. Approximately 1,000,000 colonies were grown and recovered by using Qulagen Midd prep kit. 2 micro grams of each library were used to transform DH10B cells by electroporation."
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/clone_11b="Moss EST library PPU"
/tlssue_type="protonemata: 7 day old tissue
ammonium-grown"

    519
    organism="Physcomitrella patens"

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100.0%; Pred. No.
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                                                                                                                                                                                           End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                            Zhao,S., Bass,S., Linher,K.,
E., Wible,C., Shizuya,H., Simo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 74;
5.4e+02;
                    MD 20850, USA
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                                                                                                                                                                                                                                         Shizuya, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 519;
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Simon,M. and
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ORGANISM
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VERSION
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AI314125/c
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metażoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI314125 560 bp mRNA EST 17-DEC-199 uj12e03 x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE: 1907836 3', mRNA sequence.
                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI314125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                         High quality sequence stop: 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI314125.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 301 838 0208
                                                                                                                                                                                                                                                   MGI:976032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 560)
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                                                                                                                                                                                                                         primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mdadams@tigr.org
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1. .539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="237509"
/clone_lib="CIT-HSP"
                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:1907836"
                                                                                                                              /organism="Mus musculus"
/strain="C57BL"
             /dev_stage="adult"
/lab_host="DH108"
                                                       /sex="female"
                                                                     /clone_lib="Sugano mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Sperm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
                                                                                                                                                                                     ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:4029368
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Pred. No.
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5.5e+02;
ches 0;
                                                                         kidney mkia"
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RESULT 14
AZ018937/c
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ORIGIN
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AUTHORS
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JOURNAL
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Best Local
                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 caatagaagccatg 14
                                                                                                                                                                                                                                                Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong pletcrédejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com): BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 298 row: P column: 23
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ018937 561 bp DNA GSS 25-FEB-2000
RPCI-23-298P23.TV RPCI-23 Mus musculus genomic clone RPCI-23-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Dec 15, 1999 this sequence version replaced gi:4575467. Other_GSSs: RPCI-23-298P23.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse BAC End Sequences from Library RPCI-23 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao, S., Nierman, W., Feldblyum, T., Malek, J., (Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Jong, P. and and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ018937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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ilarity 100.0%;
Conservative
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301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    szhao@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence.
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/note="0rgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
                                                                                                                                                                                                            Location/Qualifiers
1. .561
                                                                   /clone_lib="RPCI-23"
/sex="Female"
                                                                                                                   /db_xref="taxon:10090"
/clone="RPCI-23-298P23"
                                                                                                                                                                 /strain="C57BL/6J"
                                                                                                                                                                                    organism="Mus musculus"
                                             'lab_host="DH10B"
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Pred. No.
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. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malek, J., Shatsman, S.,
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VERSION

COMMENT

Query Match

Score 14;

DB 42;

Length 618;

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REFERENCE
AUTHORS
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BASE COUNT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/Dbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A1659892 618 bp mRNA EST 10-MAY-1999 tu011603.x1 NCI_CGAP_PT28 Homo sapiens cDNA clone IMAGE:2249765 3' similar to gb:M94556 SINGLE-STRANDED DNA-BINDING PROTEIN MITOCHONDRIAL PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index (1997) graph ished (1997) on Oct 8, 1998 this sequence version replaced gi:3728902. Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI659892.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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victors program: prostate, Vector: program (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified CDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
98568-986759, 1101192-1101959, and 1217928-1220615).
subtraction by Bento Soares and M. Fatima Bonaldo.

a 147 c 104 g 203 t 2 others
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/clone_lib="NCI_CGAP_Pr28"
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100.0%; Pred. No. 5.5e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100.08; Pred. No. 5.6ev02;
Matches 14; Connervative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 chatagangroatig 14

Db 562 CANTHOLANCICATE 549

Search completed: September 12, 2000, 22:46:55

Job time: 3787 sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20 21 22 23 24	15 16 17 18	10 11 12 13	0 7654322	Result
11333		13 13 13 13	133333	Score
100.0	100.0	100.0 100.0 100.0	100.0 100.0 100.0 100.0	Query Match
3458 3780 4190 4197 4343	1959 1970 2165 2339 2426	911 915 939 1242 1290 1290	487 904 904 906 910 911 911	Length
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HUMADRBRA RNU35448 RSB2AR RATMTA MMTCAN	RATADBC HSBARR AAU86080 IRO29222 AF047430	AF027228 AF027230 AF027231 AF022953 AF1022953 AF203386 CEPHOCAR	AF179732 AF027232 AF027251 AF027251 AF027225 AF027233 AF027226 AF027226	ID
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7.1	_	TITLE Sequence variation in 9 mitochondrial control region and its nuclear homolog JOURNAL Mol. Biol. Evol. 15 (1), 61-70 (1998) MEDITURE 98152305	S ISM	ACCESSION AF027251 904 bp DNA VRT 08-JUL-1998 AF027251 904 bp DNA VRT 08-JUL-1998 DEFINITION Cepphus grylle grylle isolate CGG-SF-0001 mitochondrial control region, partial sequence. ACCESSION AF027251 GT:3264899	Qy 1 cccaatggaagcc 13 Db 15 CCCAATGGAAGCC 27 RESULT 3	IN . ery Match st Local Sin tches 13;	/note-"common name: black guillemot" misc_feature <1>904 /note-"mitochondrial control region" /note-"mitochondrial control region" BASE COUNT 229 a 229 c 142 g 258 t 46 others		2 (bases Kidd,M.G. Direct Su Submitted	REFERENCE 1 (bases 1 to 904) AUTHORS Kidd, M.G. and Friesen, V.L. TITLE Sequence variation in the guillemot (Alcidae: Cepphus) mitochondrial control region and its nuclear homolog JOURNAL Mol. Biol. Evol. 15 (1), 61-70 (1998) MEDLINE 98152305	ACCESSION AF027232.1 GI:3264080 VERSION AF027232.1 GI:3264080 KEYWORDS Cepphus grylle arcticus. SOURCE Cepphus grylle arcticus ORGANISM Mitochondrion Cepphus grylle arcticus Eukaryota: Metazoa: Choradata; Craniata; Vertebrata; Archosauria;	RESULT 2 AF027232 AF027232 904 bp DNA LOCUS AF027232 904 bp DNA LOCUS DEFINITION Cepphus grylle arcticus isolate CGA-SD-0001 mitochondrial control region, partial sequence.	Db 328 CCCAATGGAAGCC 316

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AF027225 AF027225.1 GI:3264873
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Kidd, M.G. and Friesen, V.L.
Sequence variation in the guillemot (Alcidae: Cepphus)
mitochondrial control region and its nuclear homolog
Mol. Biol. Evol. 15 (1), 61-70 (1998)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Charadriiformes; Alcidae; Cepphus.
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Kidd,M.G. and Friesen,V.L.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-SEP-1997) Biology,
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l3; Conservative
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                                                                                                                                                                                        1 (bases 1 to 911)
Kidd, M.G. and Friesen, V.L.
Sequence variation in the guillemot (Alcidae: Cepphus)
mitochondrial control region and its nuclear homolog
Mol. Biol. Evol. 15 (1), 61-70 (1998)
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AF027226
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Sequence variation in the guillemot (Alcidae: Cepphus)
mitochondrial control region and its nuclear homolog
mol. Biol. Evol. 15 (1), 61-70 (1998)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Aves; Neognathae; Charadrilformes; Alcidae; Cepphus.
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AF027233
                                                                                                             Direct Submission Submitted (29-SEP-1997) Biology,
                                                                                                                                                                                                                                                                           Mitochondrion Cepphus grylle ultimus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Charadrilformes; Alcidae; Cepphus.
                                                                                                 K7L 3N6,
                                                                                                                                             2 (bases 1 to 911)
Kidd, M.G. and Friesen, V.L.
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<1. .>910
/organism="Cepphus grylle ultimus"
/organelle="mitochondrion"
/isolate="CGU-US-2190"
/sub_species="ultimus"
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/organelle="mitochondrion"
/isolate="CGA-SD-0002"
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236 c 141 g 271 t 30 others
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/db_xref="taxon:78224"
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AF027227
AF027227.1 GI:3264875
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AFU27228 911 bp DNA Cepphus grylle islandicus isolate CGI-FI-002B mitochondrial control region, partial sequence.
AF027228
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Kidd, M.G. and Friesen, V.L.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Charadriiformes; Alcidae; Cepphus
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/note="common name: black guillemot"
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239 c 138 g 270 t 26
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/organelle="mitochondrion"
/organelle="mitochondrion"
/isolate="CGI-FI-002A"
/sub_species="islandicus"
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237 c 137 g 266 t 41
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Mitochondrion Cepphus grylle islandicus
Eukaryota; Metazoa; Chordata; Craniata; Vert
Aves; Neognathae; Charadriiformes; Alcidae;
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Submitted (29-SEP-1997) Biology,
K7L 3N6, Canada
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Kidd, M.G. and Friesen, V.L.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neggnathae; Charadriiformes; Alcidae; Cepphus.
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Cepphus grylle mandtti isolate CGM-SV-0001 mitochondrial control
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Kidd, M.G. and Friesen, V.L.
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823. .857
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/isolate="CGI-FI-002B"
/sub_species="islandicus"
/db_xref="taxon:78226"
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228 c 138 g 268 t 50
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             /sub_species="mandtii"
/db_xref="taxon:78227"
                                              /organelle="mitochondrion"
/isolate="CGM-SV-0001"
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                                                                              /organism="Cepphus grylle
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 /note="common name:
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AF022953
AF022953.1 G
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1242)
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Sequence variation in the guillemot (Alcidae: Cepphus)
mitochondrial control region and its nuclear homolog
mil. Biol. Evol. 15 (1), 61-70 (1998)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Avea; Neognathae; Charadriiformes; Alcidae; Cepphus.
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Kidd, M.G. and Friesen, V.L.
Direct Submission
Submitted (29-SEP-1997) Biology,
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/note="mitochondrial control region"
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<1. .>939
                                                                                                                                                                                                                                                                                                                                                            /sub_species="mandti1"
/db_xref="taxon:78227"
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Cepphus grylle mandtii"
/organelle="mitochondrion"
/lsolate="CGM-SV-0002"
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Homo sapiens
Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                          Homo sapiens beta-2-adrenergic AF169225
AF169225.1 GI:5714687
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Liggett, S.B. and Green, S.A.
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LAIVEGNVLVITAIAKFERLQTVTNWFITSLACADLVMGLAVVPGAAHILMKMTFG
NFWCEFWTSIDDVLCVTASIETLCVIAVDRYFAITSPFKYQSLLTKNKARVIILMVWVIV
SGLTSFLPIQMWYRNTHQEAINCYANETCCDFFTNQAYAIASSIVSFVYPLVIMVYIV
YSRVFQEAKRQLQKIDKSEGRFHVQNLSQVEQDGRTGHGLRRSSKFCLKEHKALKTLG
ILMGTFTLCWLPFFIVNIVHVIQDNLIRKEVVILLMMIGYVNSGFNPLIYCRSPDFRI
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/note="Arg16
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/product="beta2-adrenergic receptor"
/protein_id="AAB82148.1"
/db_xref="GI:2570527"
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/db_xref="taxon:9606"
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2 (bases 1
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Rupert,J.R. and Hochachka,P.W.
Beta-2-adrenergic receptor allele frequencies in two native
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                                                                      Direct Submission
Submitted (09-NOV-1999) Zoology, University of British Columbia,
Submitted (19-NOV-1999) Zoology, University of British Columbia,
Submitted (19-NOV-1999) Zoology, University of British Columbia,
                                                                                                                                      2 (bases 1 to 1290)
Rupert, J.L. and Hochachka, P.W.
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1290)

Rupert,J.L. and Hochachka, P.W.
                                                                                                                                                                              Unpublished
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/cell_type-"lymphocyte"
/tissue_type-"blood"
/note-"isolated from a Quechua speaking native American heterozygous for a known C/T mutation"
17...1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="beta-2-adrenergic receptor"
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NFWCEFWTSIDVLCVTASIETCCVIAVDTYFAITSPFKYQSLLKKKKARVIILMVFV
YGLXSFLPIQHHWYRATHQEAINCYANETCCDFFTNQAYAISSIVSFYPFLVIMVFV
YSRVPQEAKROLQKIDNSEGREHVQNLSQVEQDGRTCHGLRASSIVSFYPFLVIMVFV
YSRVPQEAKROLQKIDNSEGREHVQNLSQVEQDGRTCHGLRASSFFCLKEHKALKTLG
IIMGTFTLCWLPFFIVNIVHVIQDNLIRKEVYILLNWIGYVNSGFNPLIYCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGYHVEQEKENKLLCEDLPGTEDFVGHQG
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/db_xref="taxon:9606"
/chromosome="5"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                             p DNA PRI 28-DEC-1999 adrenergic receptor (ADRB2) gene, complete cds.
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Pred. No. 6.3e+02;
Mismatches 0;
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65 CCCAATGGAAGCC 77
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Walker, J.E.
Direct Submission
Submitted (10-NOV-1993) J.E. Walker, MRC Lab of Molecular Biology,
Submitted (20-NOV-1993) J.E. Walker, MRC Lab of Molecular Biology,
Hills Road, Cambridge CB2 2QH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphate carrier.
Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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13; Conserv
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2 (bases I to 1340)
Runswick,M.J., Philippides,A., Lauria,G. and Walker,J.E.
Extension of the mitochondrial transport superfamily: sequences
five members from the nematode worm Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.elegans mRNA for x76113
                                                                                                                                                                                                                            DNA Seq. 4 (5), 281-291 (1994) 95102108
                                                                                                                                                                                                                                                                                      Runswick, M.J., Philippides, A., Extension of the mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  x76113.1 GI:472905
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345 c 333 g
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I IMGTFTLCWLPFFI VNI VHVI QDNLI RKEVY I LLNWI GYVNSGFNPLI YCRSPDFRI
AFQELLCLRRSSLKAYGNGYSSNGNTGEQSGY HVEQEKENKLLCEDLPGTEDFVGHQG
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NEWCEEWTSIDVLCVTASIETLCVIAVDRYFAITSPEKYQSLLTKNKARVIILMVMIV
SGLTSELPIQMHWYRATHQEAINCYANETCCDEFTNQAYAIASSIVSEYVPLVIMVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"beta-2 adrenergic receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ADRB2"
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5. .1027
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                                                                                                                                 /germline
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/db_xref="taxon:6239"
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                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                        Lauria, G. and Walker, J.E. transporter super-family: sequences
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Query Match 100.0%; Score 13; DB 12; Best Local Similarity 100.0%; Pred. No. 6.4e+02; Matches 13; Conservative 0; Mismatches 0;
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                                                                                                                           1 bp
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J03024 1 GI:202710
beta-adrenergic receptor. beta-bert, cDNA to mRNA, (library of Clontech), clone lambda-RHB-DAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primary structure of rat cardiac beta-adrenergic and muscarinic chollnergic receptors obtained by automated DNA sequence analysis: Furthur evidence for a multigene family Proc. Natl. Acad. Sci. U.S.A. 84, 8296-8300 (1987)
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEMCEBWTSIDVLCVTASIETLCVIAVDRYVAITSPERVQSLLTKNKARAVVILMVWIV
SGLTESFLTQMHWYRATHKQAIDCYAKETCCDFETNQAYAIASSIVSBYVFLVYMYEV
YSRVFQVAKROLQKIDKSEGREHAQNLSQVEQDGRSGHGLRSSSKFCLKEHKALKTLG
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yCalggvlsCgIThTaIvpldlvkcriqvnpekytgIatgfrttIaeegaralvkgwa
ptllgysagglgkfgfyeIfknvyadmlgeenaylyrtslylaasasaeffadIllap
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/db_xref="taxon:10116"
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Search completed: September 12, 2000, 23:03:24 Job time: 3996 sec

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16-MAR-1999 (first entry)
Staphylococcus aureus contig SEQ ID #2195.
Computer readable medium; vaccine; S.aureus infection; immunodetection;

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y Match Local Similarity hes 13; Conser	denature secondary structures denderious at temperatures migh enough to denature secondary structures. Claim 9; Pages 37-41; 80pp; French. The present sequence encodes a heat stable DNA polymerase from archaebacteria of the genus Pyrococcus sp. GE23. The encoded polymeras has an extremely high heat stability and can catalyse reactions at 70-90 degrees celsius. High molecular weight DNA was isolated from the bacteria, and screened with probes based on the polymerase genes of p. furiosus and Thermococcus litoralis to isolate the present sequence used to produce recombinant DNA encoding the present polymerase are used to produce recombinant DNA which is useful for nucleic acid amplification, including direct, reversed polymerase chain reaction (Pondouble-stranded matrices and PCR on matrices having secondary structures that block the process at conventional elongation temperatures. Sequence 4446 BP; 1358 A; 884 C; 1115 G; 1089 T;	Pyrococcus sp. Location/Qualifiers Key 1547. 3862 /*tag- a /product- DNA polymerase W09801567-A2. 15-JAN-1998. 10-JUL-1997; F01259. 10-JUL-1996; FR-008631. (APPL-) APPLIGENE-ONCOR SA. Cambon MA, Querellou J; WPI; 98-101062/09. P-PSDB; W60719. P-PSDB; W60719. DNA, vectors and transformed cells, useful in nucleic amplification reactions performed at temporatures had		87.7 87.7 87.7 87.7 87.7 87.7 87.7 87.7
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e	80pp; encode: genus; heat; High d with hococcus; trices; the pi	on/Qu.3862	446 ry) mera	
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Squeeze 69 BP; 19 A; 10 C; 18 G; 22 T;
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05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-S.aureus vaccines
Claim 1; Page 2172; 3271
This sequence represents
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                              The present sequence represents a nucleic acid sequence identified in the course of the invention, and expressed in lung, brain, kidney, heart muscle, liver, placenta, small intestine and activated T-cells. The specification also describes sequences encoding human homologues of the yeast RAD50, the Drosophila Septin-2 and Acyl-COA synthetase. The proteins have immunomodulatory activity. The nucleic acids and proteins can be used to identify activated T-cells in a sample constitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide(s) and proteins deristored on computer readable medium
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                                                                                                                                                                                                                                                                                     Novel human immunomodulatory poly:peptide(s) yeast RAD50 or Drosophila Septin-2 proteins Disclosure; Page 119; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        Dolganov G;
WPI; 98-481207/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human homologue; yeast RAD50; Drosophila Septin-2; Acyl-CoA synthetase; immunomodulatory activity; identification; activated T-cell; ds.
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27-FEB-1997; WO-U03159.
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l infection; scalded skin syndrome;
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    have homology

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W09850555-A2.
12-NOV-1998.
04-MAY-1998; U08985.
                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 2012; 2084pp; English.
Claim 1; Page 2012; 2084pp; English.
A computer readable medium has been developed which has recorded on it a computer readable medium has been developed which has recorded on it genome. The process is colated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins or other compounds having immunomodulatory activity. Sequence 319 BP; 96 A; 56 C; 74 G; 93 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis genome contig SEQ ID NO:836.
Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Enterococcus faecalis polynucleotides and polypu-
used to develop products for the detection of Enterococcus-
use in vaccines for prevention or attenuation of Enterococcus
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WPI; 99-045171/04.
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06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
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can be used in vaccines to prevent or attenuate an Enterococcal
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signal_peptide
                           Homo sapiens.
                                                         Vectors;
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ng Elk-L
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                                                       protein;
 Location/Qualifiers
1. .72
                                                                                                                   DNA; 1041
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100.0%; pr
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1.2e+02;
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                                                          growth; differentiation;
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             T DNA coding for neurotrophic human elk ligand cytokine - useful as probe to isolate other elk ligand sequences

Claim 7; Columns 27-30; 18pp; English.

C The present sequence encodes the human cytokine elk-ligand (elk-L),

C which binds a member of the tyrosine kinase receptor family. Elk-L

C exhibits neurotrophic and neuroprotective properties, and has a calculated mol. wt. 35180 daltons and a pI of 9.006. The elk-L

C cDNA, isolated from a human placental cDNA library, can be radiolabelled and used as a probe for isolating other mammalian

C clk-L cDNA. Elk-L can be used to treat neural tissue disorders, and as a neural culture reagent, while immunogenic fragments of elk-L can be used to generate specific anti-lk-L antibodies.
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Best Loc
Matches
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30-APR-1996.
13-NOV-1992; 977693.
13-NOV-1992; US-977693.
15-MAR-1994; US-212403.
(IMMV) IMMUNEX CORP.
Baum PR. Beckmann MP, (MPI: 96-229866/23.
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15-NOV-1993;
13-NOV-1992;
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Baum PR. Beckmann MP, Lyman S;

WPI; 94-183415/22.

P-PSDB; R55059.

New DNA encoding ligand for elk tyrosine kinase receptor - also related polypeptides, vectors, antibodies and probes, useful e.g. in studying cell differentiation or growth Claim I; Page 29; 35pp; English.

The sequence is that encoding the elk-L protein able to bind elk, a tyrosine kinase receptor. The DNA may be incorporated into vectors which can used to study the role of elk and its ligands in cell growth and differentiation.

Sequence 1041 BP; 239 A; 306 C; 309 G; 187 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                # signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurotrophic; neuroprotective; placenta; radiolabelled probe treatment; neural tissue; excito-toxicity; injury; disorder; neural culture reagent; immunogenic fragment; antibody; ss.
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Human cytokine elk-ligand (elk-L) cl
Human; cytokine; elk-ligand; elk-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
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US-977693.
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73. .1038
/*tag= c
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73. .1038
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1. .72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine kinase
  antibodies.
C; 309 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3e+02
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     187
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RESULT
T69766
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                                                                                                                                                                                                                     as neuro-protective agent

Claim 7; Columns 27-30; 18pp; English.

The present sequence encodes a human elk ligand (elk-L) protein,

which binds elk, has a calculated molecular weight of 35180 and an

isoelectric point of 9.006. Elk-L is a cytokine that can be used to

test cells for elk expression, measure the biological activity of

celk, purify elk by affinity chromatography and as a neuroprotective

agent to treat diabetic, hereditary and nutritional neuropathies

and neurodegenerative diseases. It may also be added to tissue

cultures to prolong the life of neurons. The elk-L cDNA was

isolated from a human placental cDNA library, and is present as a

CDNA insert in the recombinant vector deposited in strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Ma
Best Loc
Matches
                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                         Matches
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15-MAR-1994;
01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human elk ligand cDNA.
Human; elk; ligand; elk-L; cytokine; testing; measur
purification; neuroprotection; treatment; diabetic;
nutritional; neuropathy; neurodegenerative disease;
tissue culture; ss.
 Human elk-L coding sequence.
Human; elk-L; cytokine; liga
extracellular domain; immuno
                                             T97976;
                                                                                                                                                                                                                                                                                                                                                                                          (IMMV) IMMUNEX CORP
Baum PR, Beckmann MI
WPI; 97-271366/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5627267-A.
06-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signal_peptide
                                  06-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Human elk ligand protein -
                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T69766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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12; Conserv
                                                        standard;
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                                                                                                                                                        l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 W19249
                                                                                                                                                                                                               1041
                                                                                                                                                       92.3
illarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                           977693.
US-977693.
US-213403.
US-458077.
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73. .1038
/*tag= c
                                                                                                                                                                                                               BP;
                                                        CDNA
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                                                                                                               424
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immunoglobulin;
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                                                          mRNA;
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Pred. No.
                                                                                                                                                        Pred. No. 1.3
0; Mismatches
                                                         1041
tyrosine kinase receptor; fusion protein; bulin; neurological disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                              306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          testing; measuring;
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                                                                                                                                                      DB 1;
J. 1.3e+02;
O;
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1.3e+02;
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                                                                                                                                                                                                             309
                                                                                                                                                                                                                                                                                                                                                                      therapeutic
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                                                                                                                                                                             Length 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hereditary;
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                                                                                                                                                                                                                                                                                                                                                                      use,
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Best Local
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                                                      15-MAR-1994; US-213403.
13-NOV-1992; US-977693.
02-JUN-1995; US-460741.
12-NOV-1996; US-747240.
(IMMV) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-SEP-1997.
02-JUN-1995;
15-MAR-1994;
13-NOV-1992;
02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soluble fusion proteins of human elk-ligand and Fc immunoglobulin fragment - and their dinmers and oligomers, useful as neuro-protectants and neurotrophic agents

Example 3; Columns 27-30; 18pp; English.

This is the nucleotide sequence encoding the human elk-L protein, a new cytokine that is the ligand for the elk tyrosine kinase receptor. The extracellular domain of the protein (amino acids 1-213) is used to generate a fusion protein comprising the Fc polypeptide of the human immunoglobulin Gl (extending from the hinge region to the C-terminus). The fusion protein (which has the same activities as the natural elk-L protein) has neuroprotective and neurotrophic activity so is potentially useful for treating a wide range of neurological diseases.

Sequence 1041 BP; 239 A; 306 C; 309 G; 187 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
CDS
                                                                                                                                                                                                                                                                                                    V15226;
V15226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baum PR, Beckmann MP, WPI; 97-479524/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; W36055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5670625-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sig_peptide
                     Baum PR, Beckmann MP, Lyman WPI; 98-206621/18. P-PSDB; W44323.
                                                                                                                            US5728813-A.
17-MAR-1998.
                                                                                                                                                                         mat_peptide
                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                     Human elk-L encoding cDNA.

Human; elk-L; elk ligand; cytokine; antibody; cell surface receptyrosine kinase receptor; neural disease; trophic mechanism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                         27-MAY-1998
  receptors,
             Antibodies
                                                                                                                                                                                                                                            Homo
                                                                                                               12-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                      413
                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                      CCAATGGAAGCC 424
                                                                                                                                                                                                                                                                                                                                                                                            ccaatggaagcc
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                                                                                                                                                                                                                                                                                                              standard; cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
  useful
             to elk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 460741.
; US-213403.
; US-977693.
; US-460741.
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                        (first entry)
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73. .1038
/*tag= c
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1. .72
                                                                                                                                                            /*tag= a
1. 72
/*tag= b
73. 1038
/*tag= c
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1. .1041
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 ligand polypeptides for treating neural
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                                                                                                                                                     "elk-L"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                1041 BP
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                  antibody; cell surface receptor;
   disease
                                                                                                                                                                                                                                                                                                                                                                                                                  1.3e+02;
hes 0;
             bind
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
              ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1041;
              tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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RESULT X13928 X13928 X1 AC X1 DT 31 DE H. KW GH KW P¢ OS H¢ FT CI
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V08374
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellulose synthase PosA3 concellulose synthase; cotton; Gossypium hirsutum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V08374 stand
V08374;
08-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Column 27-29; 17pp; English.

The present sequence encodes human elk-L (elk ligand). The present invention describes antibodies to elk-L polypeptides. The elk-L protein is known to be neuroprotective exhibiting its effect through a trophic mechanism. Examples of diseases that may be treated with elk-L include neuropathies e.g. diabetic, hereditary and nutritional neuropathies, neurodegenerative diseases and other diseases characterised by loss of function or degeneration of neurons.

Sequence 1041 BP; 239 A; 306 C; 309 G; 187 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP-875575-A2.
04-NOV-1998.
31-MAR-1998; 3
01-APR-1997; 3
                                                                                                                                  X13928 stand
X13928;
31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes a cellulose synthase of the invention. The DNA can be used for controlling cellulose synthesis in a cell by introducing the DNA into the cell, expressing RNA with a nucleotide sequence homologous to the DNA or a nucleotide sequence complementary to the DNA. The cells are prokaryotic cells i.e. acetobacterium and/or eukaryotic cells such a yeasts i.e. Saccharomyces spp., plant cells (cotton plants) and cultured cells for the control of the control of the cells i.e. acetobacterium cells (cotton plants) and cultured cells for the cells i.e. saccharomyces spp., plant cells (cotton plants) and cultured cells for the cells i.e. saccharomyces spp., plant cells (cotton plants) and cultured cells i.e. saccharomyces spp., plant cells (cotton plants) and cultured cells i.e. saccharomyces spp., plant cells (cotton plants) and cultured cells i.e. saccharomyces spp., plant cells (cotton plants) and cultured cells i.e. saccharomyces spp., plant cells (cotton plants) and cultured cells i.e. saccharomyces spp., plant cells (cotton plants) and cultured cells i.e. saccharomyces spp., plant cells (cotton plants) and cultured cells i.e. saccharomyces spp., plant cells (cotton plants) and cultured cells i.e. saccharomyces spp., plant cells (cotton plants) and cultured cells i.e. saccharomyces spp., plant cells i.e. saccha
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Aotsuka S, Hasegawa O,
WPI; 98-559440/48.
P-PSDB; W73310.
                                    GHPO protein; Helicobacter peptic ulcer disease; ss. Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA encoding cotton cellulose synthase proteins - useful controlling cellulose synthesis in prokaryotic or eukaryotic Example 5; Page 36-37; 51pp; English.
                                                                                       H. pylori GHPO GHPO protein; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells of mammals etc.
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                                                                                                                                                                                                                                                                                                                                N
                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                           standard; DNA; 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1086 BP;
                                                                                                                                                                                                                                                                                                                                                                       ilarity 100.0%;
Conservative (
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JP-083133
                                                                                                                (first entry)
PO 701 gene.
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                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                         32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashi T, Ihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stop codon given"
                                                                                                                                                                                ВP
                                                                                           infection;
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
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J. 1.3e+02;
O;
                                                                                         gastroduodenal disease; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Le
1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plants) and cultured
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294
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increasing starch content of plants, esp. potato and tomato - by introducing into genome a gene for ADP-glucose pyro-phosphorylase activity, fused to plastid transit gene

Bisclosure; Fig 5; 120pp; English.

The inventors claim a method for inc. the starch content of a plant by inc. its ADP glucose pyrophosphorylase (ADPGPP) activity. The method uses a recombinant DNA molecule encoding a fusion protein of amino-terminal plastid transit peptide and ADPGPP. The ADPGPP gene is the glg gene of E. coli Kl2, or its mutant form glg C16 (which causes accumulation of more glycogen and has higher affinity for ADP glucose in the absence of an activator). A pref. plastid transit peptide, designated CTP1, is derived from the sakubisco la gene of from the nopaline synthase (NOS) gene.

Sequence 1575 BP; 462 A; 322 C; 365 G; 426 T;
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Best Loc
Matches
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08-OCT-1998.
01-APR-1998; U06371.
29-JUL-1997; US-902615.
01-APR-1997; US-833457.
24-JUN-1997; US-881227.
                                                                                                                                                                                                                                                                                       WO9119806-A.
26-DEC-1991.
07-JUN-1991: U04036.
18-JUN-1990: US-539763.
07-JUN-1991: US-709663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases Claim 1; Page 114-116; 2054pp; English.

This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic clarer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for the production of antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
(INMR.) MERLEUX ORAVAX PASTEUR MERIEUX SERUMS.
Al-Garawi A, Kleanthous H, Miller C, Oomen RP,
WPI; 98-542293/46.
P-PSDB; W98209.
                                                                                                                                                                                                                             WPI; 92-024423/03.
P-PSDB; R20254
                                                                                                                                                                                                                                                           (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                           Potato.
                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection and diagnosis. Sequence 1516 BP; 4
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2 CCAATGGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA; 1575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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3. .1568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 A;
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Pred. No.
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,. 1.4e+02;
0;
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RESULT 13
Q80085/c
ID Q80085;
CROORS;
DT Q80085;
DE ADDGCP small subunit gene.
KW ADP-glucose-pyrophosphorylase;
KW potato; Escherichia coll; swee
KW storage; ds:
Solanum tuberosum.
FH Key Location/Quall
FT cds (**Location**)
FH Key Location**
FH Key Location**
FH Cy Location**
F
                                                                                                                                                                                                                                                                                       RESULT 14
Q85025/c
ID Q85025
FFH OK W W DAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 48-50; 72pp; English.

Chapter App-glucose-pyrophosphorylase (ADPGPP) small subunit gene (given in Q80085) was assembled by addition of sequences from the 1st exon of the genomic clone with a nearly full-length cDNA of the same gene. The primers given in Q80087-89 were used to: introduce a BgIII+NCOI site at the ATG codon to facilitate cloning into E. coll and plant expression cy vectors; to introduce a Saci 3' cloning site at the stop codon; and to remove an internal BgIII site. The assembled gene was expressed in E. coll from the recA promoter in a PrecA-gene10L cassette. An initiating ATG codon was placed using the primer given in Q80090 to express the mature gene.

Sequence 1575 BP; 460 A; 324 C; 365 G; 426 T;
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Matches 12
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Best Local (
                      enzyme engineering; c feedstuff; food; ds. Solanum tuberosum. Key Locat cds 3. .1
                                                                                                                         ADP-glucose-pyrophosphorylase small subunit gene. Potato tuber; ADP-glucose-pyrophosphorylase small subuni site-directed mutagenesis; Escherichia coli; transgenic enzyme engineering; cloning; crop improvement; ollseed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-1995 (first entry)
ADPGPP small subunit gene.
ADP-GPP considered plant;
ADP-GPP small subunit gene.
ADP-GPP; glgC; transgenic plant;
potato; Escherichia coli; sweetness; dormancy; crop improvement;
                                                                                                                                                                                                                                   Q85025;
23-SEP-1995 (first entry)
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                                                                                                                                                                                                                                                                                       standard; cDNA;
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ilarity 100.0%;
Conservative
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                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.3%;
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                                                                                                                                                                                                                                                                                          BP
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0; Mismatches
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Pred. No.
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1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .4e+02;
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RESULT
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Matches 12
J08089249-A.
09-APR-1996.
29-SEP-1994; 234612.
29-SEP-1994; JP-234612.
(MITU ) MITSUBISHI CHEM CORP.
WPI; 96-23342/24.
P-PSDB; R91947.
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18-JAN-1995.
11-JUL-1994;
12-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pyro:phosphorylase

Disclosure; Page 21-24; 35pp; English.

Disclosure; Page 21-24; 35pp; English.

The sequence represents a potato tuber ADP-glucose-pyrophosphorylase small subunit gene. The gene is modified by site-directed mutagenesis to include a BglII-NcoI site at the ATG codon, a SacI site at the stop codon, and an internal BglII site is removed. A methionine initiation codon is internal BglII site is removed. A methionine initiation codon is introduced for expression of the mature protein in Escherichia coli. The gene is cloned together with the large subunit gene (994439) (on compatible plasmids), and subjected to mutagenesis to give improved variants of the enzyme. The resulting variant genes may be expressed in an oilseed crop plant to reduce the oil content in seeds, for use in feedstuff and food recolute.
                                                                                                                                                                                                                                                                                            27-NOV-1996 (first entry)
Brevibacterium flavum MJ-233 dihydroxy acid dehydratase coding region Dihydroxy-acid dehydratase; EC 4.2.1.9; amino acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodn of seeds e.g. peanut or soybean having decreased oil content - by providing increased levels of ADP glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer_bind
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                                                                                                                                                                                                                                                                    Brevibacterium
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Barry GF, Kishore GM,
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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US-090523.
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                                                                                                                                                                                                                                                                    e; valine; Val; Coryneform flavum MJ-233.
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(primer Q85018)"
234 435
/*tag= e
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/note= "EC-2.7.7.27"
1. 14
/*tag= b
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ATG codon (primer Q85016)"
complement (1555. .1575)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 C;
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1.4e+02;
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Matches 12
                                                                                                                                   DNA fragment contg. a gene coding for di:hydroxy-acid dehydratase derived from Brevibacterium flavum MJ 233, useful for prodn. of L-isoleucine and L-valine Claim 5; Page 9-11; 12pp; Japanese. A 6 kb genomic DNA KpnI fragment containing an open reading frame (ORF) coding for dihydroxy-acid dehydratase was isolated from Brevibacterium flavum MJ-233. The sequence of the 1836 bp ORF was determined (i.e. the present sequence) and was found to encode a protein of 612 amino acids. The enzyme is involved in biosynthesis of the amino acids isoleucine and valine.
   438
cccaatggaagc 12
                                                              l Similarity
12; Conserv
                                                              Conservative
                                                        92.3%; >--
100.0%; Pr
.-- 0;
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                                                         DB 1;
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Search completed: September 12, 2000, 23:07:26 Job time: 4108 sec

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Sequence Sequence

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23, Appl
109, App
106, App
116, Appl
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118, Appl
119, Appl

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Total number of hits satisfying chosen parameters:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1/

3: /cgn2_6/ptodata/1/

4: /cgn2_6/ptodata/1/
5: /cgn2_6/ptodata/1/
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7: /cgn2_6/ptodata/1/
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length: 1000000
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     US-08-592-126-126
US-08-413-4(03-1)
US-08-428-077-1
US-08-460-741-1
US-08-490-523-7
US-08-398-627-7
US-08-398-627-7
US-08-468-036-7
PCT-US94-05275-7
PCT-US94-05275-7
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US-08-468-036-2
US-08-458-831-19
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US-08-049-061-10
US-08-049-061-27
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US-08-049-061-12
US-08-049-061-13
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                                                                                                                                                                                                                                                                                                                                         126,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 136, Application US/08592126
Patent No. 5821091
GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Transcripts Encodi
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
US-08-592-126-126/c
                                                                      ; INDIVIDUAL ISOLATE: US-08-592-126-126
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     Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                   TELEPHONE: (415) 324-
TELEFAX: (415) 324-09
INFORMATION FOR SEQ ID NO:
                                                                                              MOLECULE TYPE: C
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 319 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 4600-01111
TELECOMMUNICATION INFORMATION:
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CITY: Palo Alto
STATE: CA
                                                                                                                                                     TOPOLOGY:
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CLASSIFICATION: 435
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US-08-463-115-10
US-08-463-115-10
US-08-136-993-11
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PCT-US95-07289-8
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RESULT 3
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US-08-213-403-1
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US-08-213-403-1
Sequence 1, Application US/08458077
                                                                                                                                                      Query Match
Best Local
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                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET MUMBER: 2807
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 233-064
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lyman, Stewart D. APPLICANT: Beckmann, M. Patricia
                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                            413 CCAATGGAAGCC 424
                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/OFFILING DATE: 15-MAR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 51 Uni
                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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12; Conserv
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|VENTION: No. 5512457el Cytokine Designated elk Ligand
|POHENCES: 2
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Carpenter, Melissa
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233-0644
233-1644
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                                                                                                                                       Score 12; DB 1; Le; Pred. No. 1.2e+02; 0; Mismatches 0;
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                                                                                                                                                                   Length 1041;
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                                                                                                                                        0;
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US-08-460-741-1 RESULT

Sequence 1, Application US/08460741 Patent No. 5670625

GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R

APPLICANT: APPLICANT:

Carpenter, Melissa

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                                                                                                                                   ; LOCATION:
US-08-458-077-1
                                                          Matches
                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2807
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 587-0
TELEFAX: (206) 233-064
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
APPLICATION NUMBER: US 07/977,693
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lyman, Stev
APPLICANT: Beckmann, N
APPLICANT: Baum, Peter
APPLICANT: Carpenter,
                                                                                                                                                                           LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                              MOLECULE TYPE:
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NUMBER OF SEQUENCES:
413 CCAATGGAAGCC 424
                                                                                                                                                                                                                                     ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple S
                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                TOPOLOGY:
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                2 ccaatggaagcc
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                                                            12;
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                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                         1041 base pairs
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                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: Apple System 7.1 Microsoft Word for Apple, Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beckmann, M. Patricia
Baum, Peter R
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100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
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                                                                                      DB 1; Length 1041;
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TITLE OF INVENTION:

5670625el Cytokine Designated elk Ligand

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RESULT
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US-08-460-741-1
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                                                                                                                                Sequence 1, Applic
Patent No. 5728813
GENERAL INFORMATI
                                                                                                                                                                                                                                                                                       Query Match 92.3
Best Local Similarity 100.
Matches 12; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,403
FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft WO CURRENT APPLICATION DATA:
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NAME: Seese, Kathryn A.
RECISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 28
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CORRESPONDENCE ADDRESS:
                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: cD
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                                                          FITLE OF INVENTION:
                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                   413 CCAATGGAAGCC 424
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OPERATING SYSTEM: Apple St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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              ADDRESSEE:
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                                                                                                                               INFORMATION:
                                                                                                                                                          Application US/08747240
E: Immunex Corporation
51 University Street
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                                                                                   Beckmann, M.
Baum, Peter R
                                                                      Carpenter, Melissa
                                                                                                              Lyman, Stewart D.
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                                            No. 5728813el Cytokine Designated elk Ligand
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                                                                                                    Patricia
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3. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Stark, David M.
APPLICANT: Stark David M.
TITLE OF INVENTION: Enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 587-0
TELEFAX: (206) 233-064
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
NAME: Seese, Wilmber: 32,172
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                           NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (206) 587-0430
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
                                                                              STREET: 700 Ches
CITY: St. Louis
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FILING DATE: 15-MAR-1994
APPLICATION NUMBER: US 07/977,693
FILING DATE: 13-NOV-1992
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                                    ZIP: 63198
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                                                 COUNTRY:
                                                                STATE: Missouri
                                                                                                               ADDRESSEE:
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                                                                                                E: Grace L. Bonner, Monsanto Co. BB4F
700 Chesterfield Parkway No. 5498830th
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73..1038
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                                                                                                                                                               Enhanced Starch Biosynthesis
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FILING DATE:

18-JUN-1990

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Matches 12; Conserv
        APPLICATION 3-MAK-1777

CLASSIFICATION: 800

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,523

FILING DATE: 12-JUL-1993

APPLICATION NUMBER: US 07/709663

APPLICATION TOWNER: US 07/709663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 7:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Bonner Grace L.
REGISTRATION NUMBER: 32,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/709663
FILING DATE: 07-JUN-1991
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APPLICATION NUMBER:
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                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Barry, G
APPLICANT: Kishore,
APPLICANT: Stark, D
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LOCATION:
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                                                                                                                              APPLICATION NUMBER: US/08/398,627
FILING DATE: 03-MAR-1995
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                                                                                                                                                                                                                                                                          63198
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nucleic acid
DEDNESS: double
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: Missouri
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700 Chesterfield Parkway No. 5608149th
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US 07/539763
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US-08-398-627-7
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Best Local
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 1575 base pairs
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                    APPLICATION NUMBER: US 08/070,155
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zalewski, James C.
TITLE OF INVENTION: Method of Improving the Quality of
TITLE OF INVENTION: Stored Potatoes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barry, Ger
APPLICANT: Kishore, C
APPLICANT: Stark, Dav
APPLICANT: Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                        REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-7286
                                                                                                                                                                                      APPLICATION NUMBER: PCT/US94/05275
FILING DATE: 18-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                         CLASSIFICATION: 800 PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Missouri
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                                                                                                          NAME: Bonner, Grace L. REGISTRATION NUMBER:
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Grace L. Bonner, Monsanto Company, BB4F 700 Chesterfield Parkway No. 5648249th
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3..1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stark, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barry, Gerard F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (314) 537-7286
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                                                                                                                                                                                                                                                                                              US/08/406,858
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                                                                                                          32,963
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                                                                                            38-21(10654)A
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LENGTH:

1575 base pairs

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; LOCATION:
US-08-406-858-7
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RESULT
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; LOCATION:
PCT-US91-04036-7
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PCT-US91-04036-7/c
                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32706
REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-7357
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application PC/TUS9104036 GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
                                                                                           Matches
                                                                                                        Query Match
Best Local S
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Best Local Similarity
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1575 base pairs
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MCB11de, Thomas P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                     FEATURE:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                               TYPE: NUCLEIC ACID STRANDEDNESS: doub TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 19910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: doub
TOPOLOGY: linear
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                                                       2 ccaatggaagcc 13
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                                                                                           12; Conservative
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Missouri
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100.0%; Pr
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                                                                                          Score 12; DB; Pred. No. 1.2
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Pred. No
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                                                                                                                       DB 6;
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Query Match
Best Local Similarity
Watches 12; Conserve
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; LOCATION:
PCT-US94-05275-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5283191 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/07912015 Patent No. 5283191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 28-MAY-1993 INFORMATION FOR SEQ ID NO: 7
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1575 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                  STREET: 1330-A FI CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Morgan, Robin Wilson
APPLICANT: Willemse, Martha Jaco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                         COUNTRY: U
ZIP: 20850
                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 CCAATGGAAGCC 8
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                            E: Biotechnology Research Institute 1330-A Piccard Drive
                                                                                                                                                                                                                                                                                                                                                          Willemse, Martha Jacoba
Claessens, Johannes Antonius Joseph
Sondermeijer, Paulus Jacobus Antonius
VENTION: Marek's Disease Virus vaccine
                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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16-NOV-1990
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                                                                                   US/07/912,015
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Pred. No. 1.2e+02;
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TELEPHONE: (301)258-5

(301)258-5200

TELECOMMUNICATION INFORMATION:

NAME: Donna Bobrowicz REGISTRATION NUMBER:

32,196

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LOCATION: 14.2005
OTHER INFORMATION:
US-07-912-015-1
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US-08-468-036-2
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08468036 Patent No. 5728806
                                                                                                                                    APPLICATION NUMBER: US 08/184
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5728806and, Greta E
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                            TELEX: 25-3856
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1224 CCCAATGGAAGC 1213
                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Narshall, O'Toole, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITLE OF INVENTION:
                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                  CLASSIFICATION:
STRANDEDNESS:
                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 06-JU
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN: GA
                                                                                         TELEFAX:
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                              ENGTH:
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              nucleic acid
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: United States
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                            2625 base pairs
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14..2005
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                                                                                                                                                                      Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                       of
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; Pred. No.
                                                                                                                                       27866/31784
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. 1.3e+02;
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                                                                              ; NAME/KEY:
; LOCATION:
US-08-376-843-2
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US-08-376-843-2
Query Match
Best Local Similarity 100.
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Best Local
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                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                          FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5846764and, Grange Gregistration Number: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
FEATURE:
                                                                                                                          FEATURE:
                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                        TELEFAX: 31-,
TELEFAX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        495 CCCAATGGAAGC 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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12; Conserv
                                                                                                                                                                                nucleic acid
                                                                                                                                                                                           2625 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Marshall, O'Toc
6300 Sears Tower,
                                                                                                                                                                                                                                                      312/474-0448
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                                                                                              CDS
796..2580
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796..2580
                                                                                                                                                     linear
                                                                                                                                                                                                                                                                    312/474-6300
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                                                                                                                                     DNA (genomic)
                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Materials and Methods Relating to Proteins that Interact with Casein Kinase I 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.3%;
100.0%;
                        92.3%; Score 12;
100.0%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anthony J. Merl F.
                                                                                                                                                                                                                                                                                                                                                                   US 08/184,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o'Toole, cower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/376,843
                                                                                                                                                                                                                                                                                                       35,302
                                                                                                                                                                                                                                                                                                                          Greta E.
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                                                                                                                                                                                                                                                                                             27866/31784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerstein, Murray & Borun South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; L
1.3e+02;
                                       DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                     Length 2625;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RESULT 14
US-08-008-216-19
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STRAIN: STRAIN A4
IMMEDIATE SOURCE:
LIBRARY: CONVOLVULUS ARVENSIS PLANT CELLS
CLONE: CLONE 7
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (937..2262)
OTHER INFORMATION: /label- ORF1SUBSEQUENCE
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Applicat
Patent No. 5366887
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 236-1048
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DALL. 800
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/725,368
APPLICATION NUMBER: 22-APR-1985
                                                                                                                                                                                                   NAME/KEY: mlsc_feature
LOCATION: complement (4041..4400)
OTHER INFORMATION: /label= ORF4SUBSEQUENCE
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,740
REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 699-2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/008,216
FILING DATE: 25-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: RI T-DNA Promoters
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DN
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                 NAME/KEY: misc_feature
LOCATION: complement (4607..4918)
OTHER INFORMATION: /label- ORFSSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: complement (2649..3458)
OTHER INFORMATION: /label= ORF2SUBSEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 21126 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 3726..4799
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NAME/KEY: mlsc_feature
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/AGENT INFORMATIC.
Barnhorst, Marnie W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Slightom, Jerry L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRAY, CARY, AMES & FRYE
1 B Street, Sulte 1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                   /label- ORF3SUBSEQUENCE
                                                                                  ORF5SUBSEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
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RESULY L.
US-08-459-569-19
Sequence 19, Application US/08459569
Patent No. 5543501
Patent No. 5543501
Patent No. 5543501
Patent No. 5819htom, Jerry L.
APPLICANT: Tepfer, David A.
TITLE OF INVENTION: Ri T-DNA Promoters
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY, CARY, AMES & FRYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LOCATION: complement (19031..19390)
; OTHER INFORMATION: /label= ORF18SUBSEQUENC
US-08-008-216-19
                                                                                                                                                                                                                                                                                                     Db 19549 CCAATGGAAGCC 19560
                                                                                                                                                                                                                                                                                                                                                                                Query Match 92.3%;
Best Local Similarity 100.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 5143..6216
OTHER INFORMATION: /label- ORF6SUBSEQUENCE FEATURE:
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LOCATION: 15659..16210
OTHER INFORMATION: /label- ORF14SUBSEQUENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 12466..13002
OTHER INFORMATION: /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: complement (10509..11282)
OTHER INFORMATION: /label= ORF11SUBSEQUENC
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LOCATION: complement (6576..6830)
OTHER INFORMATION: /label= ORF9SUBSEQUENCE
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LOCATION: complement (5071..5643)
OTHER INFORMATION: /label- ORF/SU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: complement (18177...18743)
OTHER INFORMATION: /label- ORF17SUBSEQUENC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: complement (17737..18189)
OTHER INFORMATION: /label= ORF16SUBSEQUENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: complement (16517..17545)
OTHER INFORMATION: /label- ORF15SUBSEQUENC
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LOCATION: 6609..8888
OTHER INFORMATION: /label= ORF8SUBSEQUENCE
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9748..10044
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                                                                                                                                                                                                                                                                                                                                                                                    Score 12; DB 1; I; pred. No. 1.7e+02; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORF13SUBSEQUENC
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TELEFAX: (619) 236-1048
INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 21126 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:

NAME/KEY: misc_feature

NAME/KEY: misc_feature

1700 3726..4799
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NAME/KEY: misc_feature
LOCATION: complement (:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,216
FILING DATE: 25-UAN-1993
APPLICATION NUMBER: US 06/725,368
FILING DATE: 22-APR-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                     FEATURE:
                                                                                                                               NAME/KEY: misc_feature LOCATION: 5143.6216 OTHER INFORMATION: /lab FEATURE:
                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: complement (4607.
OTHER INFORMATION: /label= (
FEATURE:
                                                                                                                                                                                                                                                                                OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                           LOCATION: 3726..47
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Agrobacterium rhizogenes
STRAIN: STRAIN A4
IMMEDIATE SOURCE:
LIBRARY: CONVOLVULUS ARVENSIS PLANT CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 401 B Street, Suite 1700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: complement (937..2262)
OTHER INFORMATION: /label= ORF1SUBSEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Barnhorst, Marnie W. REGISTRATION NUMBER: 36,740 REFERENCE/DOCKET NUMBER: P1020US1
                                                                     NAME/KEY: misc_feature
LOCATION: complement (5071..5643)
OTHER INFORMATION: /label= ORF7SUBSEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: complement (2649)
OTHER INFORMATION: /label=
                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: complement (4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
             LOCATION:
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OTHER INFORMATION:
                                     NAME/KEY:
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(619) 236-1048
                                                                                                                                                                                                                                                                                                 complement (4041..4400)
WATION: /label= ORF4SU
                 misc_feature
6609..8888
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/label= ORF8SUBSEQUENCE
                                                                                                                                                  /label= ORF6SUBSEQUENCE
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                                                                                                                                                                                                                                                                                                     ORF4SUBSEQUENCE
                                                                                                                                                                                                                              ORF5SUBSEQUENCE
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Search completed: September 12, 2000, 23:04:42 Job time: 3949 sec

Gaps

0

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QΥ
Db 19549 CCAATGGAAGCC 19560
                                                                                                                                                                           ; NAME/KEY: misc_feature; LOCATION: complement (19031..19390); OTHER INFORMATION: /label- ORF18SUBSEQUENC US-08-459-569-19
                                                                          Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY:
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NAME/KEY:
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NAME/KEY:
LOCATION:
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LOCATION: complement (6576..6830)
OTHER INFORMATION: /label= ORF9SUBSEQUENCE
FEATURE:
NAME/KEY: misc_feature
LOCATION: 9748..10044
OTHER INFORMATION: /label= ORF10SUBSEQUENC
FEATURE:
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LOCATION: complement (16517..17545)
OTHER INFORMATION: /label= ORF158UB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 15659..16210
OTHER INFORMATION: /label- ORF14SUBSEQUENC
                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: complement (18177...18743)
OTHER INFORMATION: /label= ORF17SUBSEQUENC
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LOCATION: complement (10509..11282)
OTHER INFORMATION: /label= ORF11SUBSEQUENC
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: complement (17737..18189)
OTHER INFORMATION: /label= ORF16SUBSEQUENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: 13723..14319
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                  2 ccaatggaagcc
                                                                    ch 92.3%; Score 12; DB 1; I 1 Similarity 100.0%; Pred. No. 1.7e+02; 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
12466..13002
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ORF15SUBSEQUENC
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                                                                                                                   Length 21126;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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              em_est1: * em_est2: * em_est3: * em_est4: * em_est5: * em_est6: * em_est6: * em_est10: * em_est11: * e
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9b_est31:
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9b_est31:
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9b_est34:
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117: 118: 119: 120: 121: 122: 123: 123:

gb_gss14:*
gb_gss15:*
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gb_gss18:*
gb_gss19:*
em_gss13:*

gb_gssl3:*

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Score

Match

Length

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the number of results predicted by chance to have a than or equal to the score of the result being printed, by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                               R19461 yg25h04.r1
AW676321 833002H10
R17042 yf45f05.r2
AA788418 r7h07a1.f
AA639559 ng91f08.s
A1273955 q160g11.x
A1093637 ou83d11.s
A093637 ou83d11.s
A093637 an31a04.x
AW136253 UI-H-BII-
AW137518 UI-H-BII-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D69118 CELKO65A6F
D69345 CELKO69E9F
D69342 CELKO73EYF
AA785620 99905a1.f
AW025820 wu08c09.x
AW028366 wv08b03.x
B63027 CIT978SK-13
AW442811 EST307741
AA966772 s9b01a1.f
A1022536 ow58b03.s
AA570786 nm37e03.s
AA570786 nm37e03.s
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AW324305 U273615
AW38698 AV3869806
AV278622 AV278622
AA282475 zs90c01.s
AW698136 UXNV_073
N28122 MDB1422R MO
A1352128 GY10670.x
AW411422 fh12c03.y
AW411422 fh12c03.y
AW411424 j7h11a1.f
A1845473 UI-M-A01-A1043778 UI-M-F01-A1043778 UI-M-F01-A1043778 UI-M-F01-A1043778 UI-M-F01-A1043778 UI-M-F01-G-T00893 WEST01614 E
AW597076 sj69h12.y
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AI379962 tc81b06.x
                            ID:
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JOURNAL
COMMENT
                                                                                                                                   RESULT
AI379962
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
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KEYWORDS
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ORIGIN
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                                                   AI379962
tc81b06.x1 |
similar to |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World

Parkway Circle St. Louis, Missouri 63134 For further information

call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314

427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 164)

1 (bases 1 to 164)

Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,

Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,

Reck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,

Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,

Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,

McCann,R., Waterston,R. and Wilson,R.

Public Soybean EST Project

Unpublished (199)

On Jan 6, 2000 this sequence version replaced gi:6675643.
mRNA sequence.
AI379962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: SHOWMENT ST Project
Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine max
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Fabales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN. ;, mRNA sequence. AW396623 AW396623.1 GI:6915162 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Jan 6, 2000 this sequence version replaced Contact: Shoemaker R/Public Soybean EST Projec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fabaceae;
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     greenhouse grown plants. Complementary DNA was synthesized from mRNA using a 3' anchored poly(dT) primer. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and HindIII. The cDNA fragments were directionally cloned into the EcoRI-HindIII restriction site of the pT7T3-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRL). This library was constructed R. Shoemaker and Erpelding." 31 \ c \qquad 37 \ g \qquad 49 \ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pT7T3-Pac (Pharmacia); Site_1: EcoRI
Site_2: HindIII; This cDNA library was constructed
mRNA isolated from senecsing leave tissue of mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                grown."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Senescing leaves, mature plants, greenhouse
grown."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="GENOME SYSTEMS CLONE ID: Gm-c1026-44"
/clone_lib="Gm-c1026"
                                             175 bp ml
1 NCI_CGAP_CLL1 1
5 SW:UCRP_HUMAN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Glycine max"
/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                        Score 13; DB 71;
Pred. No. 7.8e+02;
; Mismatches 0;
                                                   mRNA EST 18-MAR-1999
Homo sapiens cDNA clone IMAGE:2072531 3'
P05161 UBIQUITIN CROSS-REACTIVE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Project
                                                                                                                                                                                                                                                                                                                                                                                                              Length 164;
                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 1
AW396623/c
                                          DEFINITION
AW396623 164 bp mrNA EST 07-FEB-ZUUU s980d10.y1 Gm-c1026 Glycine max cDNA clone GENOME SYSTEMS CLONE Gm-c1026-44 5' similar to TR:080828 080828 HYPOTHETICAL 88.8 KD
```

ALIGNMENTS

00000

AQ019463 AI367860 AI123505

AQ208746 AI050032

AW136253 AW137518

AW676321 R17042 AA788418 AA639559 AI273585 AI093637

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AA570786 AZ037328 AW442811 AA966772 AI022536

R19461

AA785620 AW025820

AW028366

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T00893 AW597076

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AV281774
AW324305
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AV278622
AA282475
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AA71643778

COMMENT

TITLE

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KEYWORDS
SOURCE
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AUTHORS
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45 CCCAATGGAAGCC 57
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Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llni.gov/bbrp/image/image.html
                                                                                                                                                                                                         AV281774 189 bp mRNA EST 05-NOV-1999 AV281774 RIKEN füll-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4933426F15 3', mRNA sequence.
AV281774
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on May 18, 1998 this sequence version replaced gi:3137165
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 189)
                                                                                                               Mus musculus
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.
                                                                                                                                                                                      AV281774.1
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48 c 34 g 46 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:2072531"
/clone_lib="NCI_CGAP_CLL1"
/tlssue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo saplens"
/db_xref="taxon:9606"
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Pred. No.
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. 7.9e+02;
ches 0;
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Best Local Similarity 100 Matches 13; Conservative

100.0%;

Score 13; Pred. No. Mismatches

8e+02; DB 60; 0

Length 189; Indels

0;

Gaps

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Query Match Best Local

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BASE COUNT
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On Apr. 7, 1998 this sequence version replaced gi:3034900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. okazaki, Y. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@rtc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: +81-298-36-9098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            further details
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                              65
                    /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                      prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="4933426F15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="testis"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RIKEN full-length enriched, adult male testis
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TITLE
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                                                                                                                                                                                                          CCCAATGGAAGCC 38
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Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Other_ESTs: uo27a01.y1
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria;
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                                                      AV386986 215 bp mRNA EST 21-JAN-2000 AV386986 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii cDNA clone CMO10g1l_r, mRNA sequence.

AV386986
Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                   Similarity
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal
site_2: NotI; Cloned unidIrectionally. Primer: Oligo of
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
a 40 c 54 g 50 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue-yee="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:2616072"
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Rodentia;
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Pred. No. 8.1e+02;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                       Length 199;
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                                                                                                                                                                             Matsuyama, T., Miki, R., Mizuno, Y., Makamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shipata, Y., Shipata, Y., Shipata, Y., Shipata, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Vohita, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Piken Mouse ESTS (Konno, H., et al.)
Unpublished (1999)
On Jul 8, 1999 this sequence version replaced gi:5420947.
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Exploration Research Group, Life Science Tsukuba Center, Genome Calence Laboratory
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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AV278622 RIKEN full-length enriched, adult male testis (DH10B) Mus
musculus cDNA clone 493340201B 3', mRNA sequence.
AV278622
                                    3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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genome-res@rtc.riken.go.jp,
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/clone_lib="Chlamydomonas reinhardtii C9"
/clone_lib="Chlamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_1:
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/strain="C9"
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Sciurognathi; Muridae; Murinae; Mus
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303
Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalla; Eutheria; Primates; Catarrhini; Hom
1 (bases 1 to 254)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
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/dev_stage="adult"
/lab_host="DH10B"
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/clone="4933402018"
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Primates;
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On Jan 14, 1998 this sequence version replaced
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NXNV_073_C07_F Nsf Xylem Normal wood
clone NXNV_073_C07 5', mRNA sequence.
                                                                                        Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
                                                                                                                                     Unpublished (2000)
                                                                                                                                                             Sederoff, R.
                                                                                                                                                                     Coniferopsida; Coni
1 (bases 1 to 293)
                                                                                                                                                                                 Eukaryota; Viridiplantae; Embryophyta; Trach
Coniferopsida; Coniferales; Pinaceae; Pinus.
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/organism="Pinus taeda"
/db_xref="taxon:3352"
/clone="NxNV_073_C07"
/clone_11b="Nsf Xylem Normal wood Vertical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:704736"
/clone_lib="NCI_CGAP_GCB1"
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/lab_host="DH10B"
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                                                                                                                                                 the Pine Megagenome
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Matches 13; Conserv
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N28122
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Unpublished (1995)
On May 14, 1999 this sequence version replaced gi:4827793.
Contact: Sikela JM
Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
Fax: 3032707097
                    AI352128 326 bp mRNA EST 13-FEB-1999 gr10f07.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1940485 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                          l Similarity
13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: nikki@tally.uchsc.edu
Insert Length: 403 Std Error:
Seq prlmer: M13 Reverse.
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Mammalia; Eutheria;
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llarity 100.0%;
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a 67 c 60 g 83 t 11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Mouse brain, Stratagene"
/lab_host="E. coli XII-Blue"
/note="Vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZAP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: EcoR I; Site_2: Xho I;
/note="Vector: Lambda ZaP; Site_1: Lambda Za
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Rodentia;
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Pred. No. 8.6
); Mismatches
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Pred. No. 8.6e+02;
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VERSION
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1 (bases 1 to 326)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 332)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: AFCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                          Unpublished (1999)
On Apr 30, 1999 this sequence version
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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EST.
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AW411422.1 GI:6936963
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fh12c03.y1 NIH_MGC_17 Homo
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Email: Robert_Straus
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                                                                          Tel: (301) 496-1550
                                                                                                                                                                                                                                                               human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="INAGE: 1940485"
/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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100.0%; F
tive 0;
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Pred. No. 8.8e+02;
Nutematches 0;
                                                                                                                                                                                                                                                                                                                                                       sapiens cDNA
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                                                                                                             replaced gi:4727490
                                                                                                                                                                                                                                                                                                                                                         EST 16-FEB-200 clone IMAGE: 2964485
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RESULT 1
AA786244
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|||||||||||||
171 CCCAATGGAAGCC 159
                                                                                                                                                                                                                                                                                                                                An Aspergillus nidulans EST Database
Unpublished (1998)
Other_ESTs: J7h1lal.rl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoman Parrington Oval, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA786244 338 bp mRNA EST 31-JUL-1998 J7hllal.fl Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Aspergillus nidulans cDNA clone J7hllal 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus nidulans
Eukaryota; Fungi; Ascomycota; Eurotiales; Trichocomaceae;
anamorphic Trichocomaceae; Aspergillus.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.linl.gov/bbrp/image/image.html
                                                                                                                                                                                          We anticipate the future release Genetics Stock Center Seq primer: M13-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA786244
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                                                                                                                                                                                                                                                                    Email: broe@ou.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kupter,D., Gray,J., Hausner,J., Lai,H.,
Prade,R. and Roe,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA786244.1 GI:2846412
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                                                                                                                                                                                                                                                                                        Parrington Oval,
405 325 4912
405 325 7762
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                                                                                                                                                                      quality sequence stop: 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="rhabdomyosarcoma"
/lab_host="0180 (phage-resitant)"
/lab_host="0180 (phage-resitant)"
/note="0798n: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Site_2: XhoI; cDNA made by oligo-dT priming using the Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAGG). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callfornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 70 c 46 g 141 t
                                                                                                                                             Location/Qualifiers
                                             /organism="Aspergillus nidulans"
/strain="FGSC A26"
/db_xref="taxon:5072"
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/clone_lib="NIH_MGC_17"
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/db_xref="taxon:9606"
/clone="j7hllal"
/clone_lib="Aspergillus nidulans 24hr asexual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Pred. No. 8.8e+02;
; Mismatches 0;
                                                                                                                                                                                                                                             of the
                                                                                                                                                                                                                                                                                                                                                               University of Oklahoma
                                                                                                                                                                                                                                             cDNA clones to the Fungal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized pineal glands library cDNA Library Preparation: M.B. soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI845473 338 bp mRNA EST 15-JUL-1999
UI-M-AO1-aej-h-05-0-UI.sl NIH_BMAP_MPG_N Mus musculus cDNA clone
UI-M-AO1-aej-h-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The following repetitive elements were found 1-30, >AT_rich#Low_complexity
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1 (bases 1 to 338)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mEST@mail.nih.gov
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301 443 9890
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/organism="Mus musculus"
/organism="Mus musculus"
/strain="057BL/63"
/db_xref="taxon:10090"
/clone=_itaxon:10090"
/clone=_itaxon:10090"
/clone=_itaxon:10090"
/dev_stage="27-32 days"
/dev_stage="27-32 days"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/lab_host="Jenes"
/lab
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/note="Vector: pBlueScript SK-; Site_1: ECORI; Site_2:
xhoI; 5' end of cDNA cloned into ECORI site of pBluescript
3' end of cDNA cloned into xhoI site of pBluescript"
a 86 c 68 g 91 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chin, H
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UI-R-CO-jm-f-10-0-UI 3', mRNA sequence.
AI043778.1 GI:3290513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the
oligo-dT track served to identify it as a clone from the normalized
adult 8-Day-Embryo library. cDNA Library Preparation: M. Fatima
Bonaldo, Ph.D. Clone distribution: clones will be available through
Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
ID-1783157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Jun 5, 1998 this sequence version replaced gi:3189294 Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 348)
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/ub_nost="bullow (Life Technologies)"
/lab_host="bullow (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CO-jm-f-10-0-UI"
/clone_lib="UI-R-CO"
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8.8e+02;
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1 cccaatggaagcc 13
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McCombie,W.R., Kelley,J.M., Aubin,L., Goscoechea,M.,

FitzGerald,M.G., Wu,A., Adams,M.D., Dubnick,M., Kerlavage,A.R.,

Venter,J.C. and Fields,C.A.

Caenorhabditis elegans cDNAs

Opublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic 1 9712 Medical Center Drive, Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 5, 1995 this sequence version replaced g1:798322 Other_ESTs: wEST01615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                       Email: arkerlav@tigr.org
Insert Length: 1663 Sto
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kerlavage, AR
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                                                              Similarity
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                                                                                                                                                          89
                                            Conservative
                                                                                                                                                      /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone="CEESK50"
/clone=11b="EBITIY embryo, Stratager
/clone_11b="EBITIY embryo, Stratager
103 c 72 g 84 t 2
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Pred. No. 8.9e+02;
, Mismatches 0;
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Rockville,
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